

INTERNATIONAL SEARCH REPORT

Inte: Application No
PCT/US 00/25856

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/54 C12N9/10 C12N15/82 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, STRAND, BIOSIS, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EMBL Database, Heidelberg, FRG Empln accession number AB023482 15 March 1999 SASAKI, T. ET AL.: "Oryza sativa genomic DNA, chromosome 6, clone P0680A03" XP002167058	1,3,4
Y	the whole document	2
X	EMBL Database, Heidelberg, FRG Empln accession number AB020755 14 December 1998 NAKAMURA, Y.: "Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1" XP002160876	1,3
Y	the whole document	2,4
	-/-	

☒ Further documents are listed in the continuation of box C.

☐ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *G* document member of the same patent family

Date of the actual completion of the international search

10 May 2001

Date of mailing of the international search report

28.05.01

Name and mailing address of the ISA

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INTERNATIONAL SEARCH REPORT

Inte Application No
PCT/US 00/25856

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EMBL Database, Heidelberg, FRG Empln accession number AB011483 10 March 1998 NAKAMURA, Y.: "Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9" XP002160878 cited in the application	1,3
Y	the whole document	2,4
X	EMBL Database, Heidelberg, FRG Empln accession number AC007584 19 May 1999 LIN, X. ET AL.: "Arabidopsis thaliana chromosome II section 101 of 255 of the complete sequence. Sequence from clones MJB20, T19E12" XP002167059	1,3
Y	the whole document	2,4
X	EMBL Database, Heidelberg, FRG Emest_Pln2 accession number AI965398 24 August 1999 SHOEMAKER, R. ET AL.: "sc71b10.y1 Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1016-1844 5' similar to SW: Y506_SYNY3 Q55482 HYPOTHETICAL 28.8 KD PROTEIN SLL0506, mRNA sequence" XP002167060	1,3
Y	the whole document	2,4
X	EMBL Database, Heidelberg, FRG Emest_Pln2 accession number AU069089 07 June 1999 SASAKI, T.: "Oryza sativa cDNA, partial sequence (C52041_1A)" XP002160877	1
A	the whole document	13-15
X	EMBL Database, Heidelberg, FRG Emest_Pln4 accession number AW038635 17 September 1999 D'ASCENZO, M. ET AL.: "EST280318 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA clone cLET7I9, mRNA sequence" XP002167061	1
A	the whole document	13-15

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INTERNATIONAL SEARCH REPORT

Intel. of Application No.

PCT/US 00/25856

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	APFEL, C.M. ET AL.: "Use of Genomics To Identify Bacterial Undecaprenyl Pyrophosphate Synthetase" JOURNAL OF BACTERIOLOGY, vol. 181, no. 2, January 1999 (1999-01), pages 483-492, XP002160874 cited in the application	2,4
A	abstract page 486 -page 487; figure 3 page 488, column 1, line 7 -column 2, line 3 page 490, column 2, line 36 - line 64	1,3,5-15
A	SHIMIZU, N. ET AL.: "Molecular Cloning, Expression, and Purification of Undecaprenyl Diphosphate Synthase" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 273, no. 31, 31 July 1998 (1998-07-31), pages 19476-19481, XP002160875 cited in the application the whole document	1-15
A	DATABASE BIOSIS 'Online! BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; PHYTOCHEMICAL ANALYSIS, vol. 8, no. 3, 1997 CORNISH, K. & BARTLETT, D.L.: "Stabilisation of particle integrity and particle bound cis-prenyl transferase activity in stored, purified rubber particles" XP002161336 abstract	1-15

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/25856

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☒ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-15 partially

An isolated nucleic acid fragment encoding a plant cis-prenyltransferase polypeptide selected from the group consisting of a) an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence SEQ ID NO: 2, b) an isolated nucleic acid fragment that is substantially similar to an isolated nucleic acid fragment encoding all or a substantial portion of SEQ ID NO: 2, c) an isolated nucleic acid fragment derived from *Dimorphotheca* encoding a polypeptide having at least 41% identity with the amino acid sequence SEQ ID NO: 24, d) an isolated nucleic acid fragment derived from *Dimorphotheca* having at least 50% identity with the nucleic acid sequence SEQ ID NO: 23, e) an isolated nucleic acid fragment that hybridizes with said nucleic acid sequences, f) an isolated nucleic acid fragment that hybridizes with the nucleic acid sequence SEQ ID NO: 1, g) an isolated nucleic acid fragment that is complementary to said nucleic acid sequences, said isolated nucleic acid fragment having the nucleic acid sequence SEQ ID NO: 1, a polypeptide encoded by said isolated nucleic acid fragment, said polypeptide having the amino acid sequence SEQ ID NO: 2, a method of obtaining a nucleic acid fragment encoding all or a substantial portion of the amino acid sequence of a plant cis-prenyltransferase polypeptide comprising a hybridization step involving said nucleic acid fragment, a method of obtaining a nucleic acid fragment encoding all or a substantial portion of the amino acid sequence of a plant cis-prenyltransferase polypeptide comprising a cDNA amplification step involving primers corresponding to a portion of SEQ ID NO: 1, a chimeric gene comprising said nucleic acid fragment, a transformed host cell comprising said chimeric gene and a method of altering the level of expression of a plant cis-prenyltransferase polypeptide in a host cell;

2. Claims: 1-15 partially

Idem as subject 1 but limited to *Calendula officinalis* and SEQ ID NOS: 3 and 4;

3. Claims: 1-15 partially

Idem as subject 1 but limited to *Hevea brasiliensis* and SEQ ID NOS: 5-10;

4. Claims: 1-15 partially

Idem as subject 1 but limited to *Vitis* sp. and SEQ ID NOS:

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

11 and 12;

5. Claims: 1-15 partially

Idem as subject 1 but limited to Oryza sativa and SEQ ID NOS: 13-16;

6. Claims: 1-15 partially

Idem as subject 1 but limited to Glycine max and SEQ ID NOS: 17 and 18;

7. Claims: 1-15 partially

Idem as subject 1 but limited to Triticum aestivum and SEQ ID NOS: 19 and 20.

1/24

Polyprenol biosynthesis

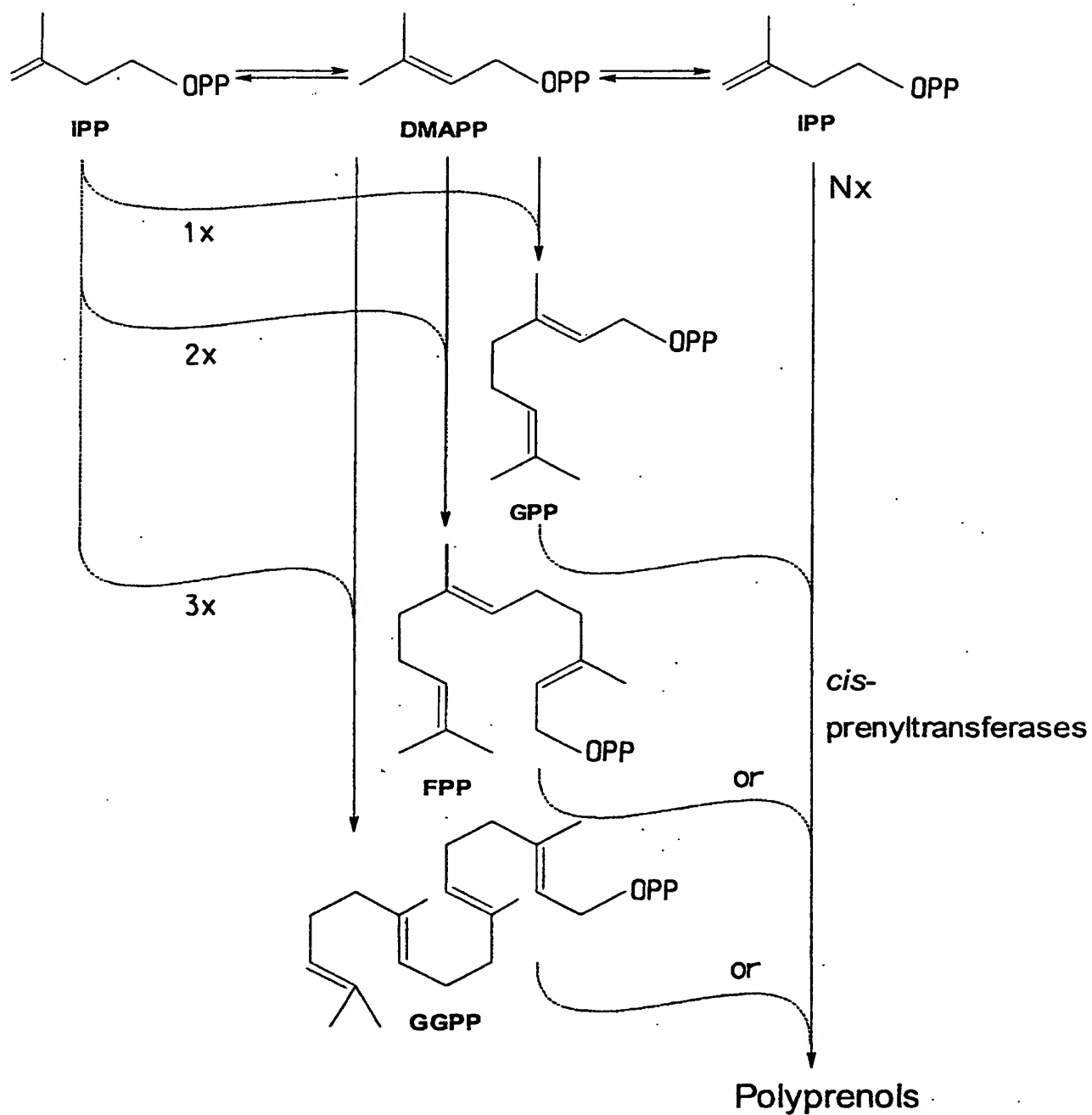


FIG. 1

3/24

ecs1c.pk009.p19 (SEQ ID NO:3) -----
 ehb2c.pk001.i10 (SEQ ID NO:5) -----
 ehb2c.pk001.d17 (SEQ ID NO:7) -----
 ehb2c.pk001.o18 (SEQ ID NO:9) -----
 r10n.pk117.i23 (SEQ ID NO:13) -----
 rr1.pk005.h8 (SEQ ID NO:15) -----
 s11.pk0128.h7 (SEQ ID NO:17) -----
 vdb1c.pk001.k23 (SEQ ID NO:11) -----
 wdk5c.pk005.f22 (SEQ ID NO:19) -----
 M.lutupps (SEQ ID NO:23) -----
 yeast rer2 (SEQ ID NO:25) -----
 yeast srl1 (SEQ ID NO:27) -----
 (19) -----
 (1) -----
 (1) -----
 (1) -----
 (1) -----
 (1) -----
 (1) -----
 (1) -----
 (101) ATC--ATCCTTTCCATCACCGTTCCCAAAACACAGAGTCTTATCGTCTCGA
 (86) ACAGAATCGATTCAATTTCTTTTCCCTCCAATCTCAGTTCACAGATTTCAC
 (1) -----
 (1) -----
 (1) -----
 (1) -----
 (31) TTTGTAGCCCTAAAAAGGCTTTTGGTAGAAACCAAGAACACAGATGTGCTT

dms2c.pk005.c7 (SEQ ID NO:1) -----
 ecs1c.pk009.p19 (SEQ ID NO:3) -----
 ehb2c.pk001.i10 (SEQ ID NO:5) -----
 ehb2c.pk001.d17 (SEQ ID NO:7) -----
 ehb2c.pk001.o18 (SEQ ID NO:9) -----
 r10n.pk117.i23 (SEQ ID NO:13) -----
 rr1.pk005.h8 (SEQ ID NO:15) -----
 s11.pk0128.h7 (SEQ ID NO:17) -----
 vdb1c.pk001.k23 (SEQ ID NO:11) -----
 wdk5c.pk005.f22 (SEQ ID NO:19) -----
 M.lutupps (SEQ ID NO:23) -----
 yeast rer2 (SEQ ID NO:25) -----
 yeast srl1 (SEQ ID NO:27) -----
 (53) CTCT---CTCCACCAACCACCACCGTGGTCTTTATGTATTCAACCAATCA
 (1) -----
 (1) -----
 (1) -----
 (1) -----
 (1) -----
 (1) -----
 (1) -----
 (1) -----
 (22) TACTTACCTTCAGTGGATTCAAAGACGGAGACACTGATGAGTTAATTTC
 (149) AGCGGGTTCCGCCATTGCGAAGTGTACGCTGATAGCGTGACACTTCCT
 (136) AAA---CTTCGC-ACAGCTAAAACTGATGTAG-----TTGGG
 (1) --A---TGCCGC-TCTCC-AACTCT-ACGTCG-----TCTGT
 (1) -----
 (1) -----
 (1) -----
 (81) CGCA--GTGAAAGTATATTTCAGAGAGTATTGCGTGGGTTATGTCAT

dms2c.pk005.c7 (SEQ ID NO:1) -----
 ecs1c.pk009.p19 (SEQ ID NO:3) -----
 ehb2c.pk001.i10 (SEQ ID NO:5) -----
 ehb2c.pk001.d17 (SEQ ID NO:7) -----
 ehb2c.pk001.o18 (SEQ ID NO:9) -----
 r10n.pk117.i23 (SEQ ID NO:13) -----
 rr1.pk005.h8 (SEQ ID NO:15) -----
 (100) GACCACTGGAGGTGGAAATTAATTCGCTGGGACCGCTTACTCCGCG
 (1) -----
 (26) CAGTGTGTTTCAGACT--TTTAGGAGTATGAGATGAGGTTATT
 (26) CAGTGTGTTTCAGACT--TTTAGGAGTATGAGATGAGGTTATT
 (26) CAGTGTGTTTACAAT--TTTGGGAAATACATGAGATGAGGTTATT
 (1) -----
 (72) GACTGGTGTTCCTGCTAGTCTGCAATTTCTCCGCTAATGCATTGTAG

FIG. 2-2

4/24

FIG. 2-3

SUBSTITUTE SHEET (RULE 26)

sll.pk0128.h7	(SEQ ID NO:17)	(199)	GATACGGAGTCTCGCTGCGCCCAAGTGTGTTGAGCCACAT---CCGGC
vdb1c.pk001.k23	(SEQ ID NO:11)	(169)	GAGGAAGAAGCAAGAGAAGTAAACAGAGAGCGGCTGATAT---CCGG
wdk5c.pk005.f22	(SEQ ID NO:19)	(30)	GCGG---GCCGTACCGTCCCGCGCGCGGCTCCGCTCCGCTCC
M.lutupps	(SEQ ID NO:23)	(1)	-----ATGTTTCCAATTAGAGCGGAAAGCAATAAAAAT
yeast rer2	(SEQ ID NO:25)	(21)	ACCTGGTCATTCATTTGTATAAGTGGACATAAATACATCTTTTCGGCA
yeast srl1	(SEQ ID NO:27)	(128)	TAGCTTGTTTTCATGG-TTATATATAAATCTTCAGATATTTTGGATAA
dms2c.pk005.c7	(SEQ ID NO:1)	251	AGGAG-CAAGCACAGTATAATCCAAAGATGCGAGTGAATCTGGAT
ecs1c.pk009.p19	(SEQ ID NO:3)	(150)	-----TCCAAATACCTTGGATTAATATGGAT
ehb2c.pk001.i10	(SEQ ID NO:5)	(74)	GCATCCAAACCCACGCTCCCTCCGTAATCAATATGGCTTATATGGAT
ehb2c.pk001.d17	(SEQ ID NO:7)	(74)	GCATCCAAACCCACGCTCCCTCCGTAATCAATATGGCTTATATGGAT
ehb2c.pk001.o18	(SEQ ID NO:9)	(74)	GCATCCAAACCCACGCTCCCTCCGTAATCAATATGGCTTATATGGAT
r10n.pk117.i23	(SEQ ID NO:13)	(1)	-----TCCAAAGCAATATGGATTTATATGGAT
rr1.pk005.h8	(SEQ ID NO:15)	(122)	CTGTCTCTCGTATGCGCAATCCCTTAAAGCAATATGGATTTATATGGAT
sll.pk0128.h7	(SEQ ID NO:17)	(246)	GGAAG-TCGCGCGGAGATGTTCCGAAAGATGCTGCGGTGATATGGAC
vdb1c.pk001.k23	(SEQ ID NO:11)	(216)	CGGTG-ATCGGAGAGAAATGATCCGGAAATCGTGGCGTATATGGAC
wdk5c.pk005.f22	(SEQ ID NO:19)	(72)	AGGGG-TCGCGGCGAGTCGCTCCGCGGATCGTGGCGTGGTATGGAC
M.lutupps	(SEQ ID NO:23)	(38)	ATAAATAATGCGCAAAATTCGGAAATCAATATGGAAATATATGGAC
yeast rer2	(SEQ ID NO:25)	(71)	CATTGCGTGCATCTAACTGTGATCTAGCAATGTTGGTTATATATGGAT
yeast srl1	(SEQ ID NO:27)	(177)	AGCAT-TAAGGGTAGGCGCAGTCCCTGAAATCTCTCTTATATATGGAT
dms2c.pk005.c7	(SEQ ID NO:1)	301	CGAAGAGGAGTGGCGTCGATCACGTCGTTAATGCGCGATGCTGGTATA
ecs1c.pk009.p19	(SEQ ID NO:3)	(31)	CGAAGCCTCTGTTGGCGGTGGAAAGCTGTGTCTCCATGACCGGGA
ehb2c.pk001.i10	(SEQ ID NO:5)	(124)	CGAAGAGGAGGCTTGGTAAGAGCTTAACTGGGAAAGGAGGTGGTGA
ehb2c.pk001.d17	(SEQ ID NO:7)	(124)	CGAAGAGGAGGCTTGGTAAGAGCTTAACTGGGAAAGGAGGTGGTGA
ehb2c.pk001.o18	(SEQ ID NO:9)	(124)	CGAAGAGGAGGCTTGGTAAGAGCTTAACTGGGAAAGGAGGTGGTGA
r10n.pk117.i23	(SEQ ID NO:13)	(31)	CGTAACCTTCAATATGCTTAATTCGGAGTATCCAGAAAGGCTCTGGTGA
rr1.pk005.h8	(SEQ ID NO:15)	(172)	GGTAACCTTCAATATGCTTAATTCGGAGTATCCAGAAAGGCTCTGGTGA
sll.pk0128.h7	(SEQ ID NO:17)	(295)	GGGAAAGGAGGCTTGGCGAGTGAAGGCTTGGACCTCCGCGGGGA
vdb1c.pk001.k23	(SEQ ID NO:11)	(265)	GGGAAAGTGAAGGCTTGGCGAGTGAAGGCTTGGCGCGCTCGGGTGA
wdk5c.pk005.f22	(SEQ ID NO:19)	(121)	GGGAAATCCGCTGGCGGAGCGCGGCGCTTGGCGCGGACGACGGGA
M.lutupps	(SEQ ID NO:23)	(88)	GGAAATGGCCATGGGCAATACAGAAATAATGGCGGCATAAAAGGAGA
yeast rer2	(SEQ ID NO:25)	(121)	GGGAAAGGAGGCTTGGTAAGAGCTTAACTGGGAAAGGAGGTGGTGA
yeast srl1	(SEQ ID NO:27)	(226)	GGTAACCGGAGATATGCCAAGTCAAGAGGCTTAACTTAAAAAAGGCGA

5/24

351
dms2c.pk005.c7 (SEQ ID NO:1) 400
ecslc.pk009.p19 (SEQ ID NO:3)
ehb2c.pk001.i10 (SEQ ID NO:5)
ehb2c.pk001.d17 (SEQ ID NO:7)
ehb2c.pk001.o18 (SEQ ID NO:9)
r10n.pk117.i23 (SEQ ID NO:13)
rrl.pk005.h8 (SEQ ID NO:15)
sll.pk0128.h7 (SEQ ID NO:17)
vdb1c.pk001.k23 (SEQ ID NO:11)
wdk5c.pk005.f22 (SEQ ID NO:19)
M.lutupps (SEQ ID NO:23)
yeast rer2 (SEQ ID NO:25)
yeast srl1 (SEQ ID NO:27)

(249) CATGGAAGCTGCACGCTCATTTGAGGTGATGGGGAATGCTCGTAA
(81) TAGTGGCATGAGAAAGAGGCTCAATCTCCCTTTTCGAGTTCCTCA
(174) TAAAGCTGCAATTTTAGGCTCTGACGGAAGAACTTATGGATGCG
(174) TAAAGCTGCAATTTTAGGCTCTGACGGAAGAACTTATGGATGCG
(174) TAAAGCTGCAATTTTAGGCTCTGACGGAAGAACTTATGGATGCG
(81) GAGCTGCGCTCTCTGCTGCTCAATGCGGCTCTCTACGCTATGAA
(222) GAGCTGCGCTCTCTGCTGCTCAATGCGGCTCTCTACGCTATGAA
(345) GCGGCTGCGGCTGCAATGCTGAGGCTGCTGAGAGCTGCTGCA
(315) GCTGAGCTGCGGCTGCAATGCTGAGGCTGCTGAGAGCTGCTGCA
(171) GGCACGCTGCGGCTGCAATGCTGAGGCTGCTGAGAGCTGCTGCA
(138) TTTGAACTGCGGCTGCAATGCTGAGGCTGCTGAGAGCTGCTGCA
(171) GAGGCTGCGGCTGCAATGCTGAGGCTGCTGAGAGCTGCTGCA
(276) TGAAGCTGCGGCTGCAATGCTGAGGCTGCTGAGAGCTGCTGCA

401
dms2c.pk005.c7 (SEQ ID NO:1) 450
ecslc.pk009.p19 (SEQ ID NO:3)
ehb2c.pk001.i10 (SEQ ID NO:5)
ehb2c.pk001.d17 (SEQ ID NO:7)
ehb2c.pk001.o18 (SEQ ID NO:9)
r10n.pk117.i23 (SEQ ID NO:13)
rrl.pk005.h8 (SEQ ID NO:15)
sll.pk0128.h7 (SEQ ID NO:17)
vdb1c.pk001.k23 (SEQ ID NO:11)
wdk5c.pk005.f22 (SEQ ID NO:19)
M.lutupps (SEQ ID NO:23)
yeast rer2 (SEQ ID NO:25)
yeast srl1 (SEQ ID NO:27)

(299) GGGGATCTAGTCCCTATGCTGTTGCTTCCCTTCGAGCTGATACCTGGTTA
(131) GCAATCTAGGCGGATGATTTATGGAATTTGCTACCGAATTTGGA
(224) TAAAGCTGCAATTTTAGGCTCTGACGGAAGAACTTATGGATGCG
(224) TAAAGCTGCAATTTTAGGCTCTGACGGAAGAACTTATGGATGCG
(224) TAAAGCTGCAATTTTAGGCTCTGACGGAAGAACTTATGGATGCG
(131) GGGGATCTAGTCCCTATGCTGTTGCTTCCCTTCGAGCTGATACCTGGTTA
(272) GGGGATCTAGTCCCTATGCTGTTGCTTCCCTTCGAGCTGATACCTGGTTA
(395) GGGGATCTAGTCCCTATGCTGTTGCTTCCCTTCGAGCTGATACCTGGTTA
(365) GGGGATCTAGTCCCTATGCTGTTGCTTCCCTTCGAGCTGATACCTGGTTA
(221) GGGGATCTAGTCCCTATGCTGTTGCTTCCCTTCGAGCTGATACCTGGTTA
(188) TAAAGCTGCAATTTTAGGCTCTGACGGAAGAACTTATGGATGCG
(221) TAAAGCTGCAATTTTAGGCTCTGACGGAAGAACTTATGGATGCG
(326) TAAAGCTGCAATTTTAGGCTCTGACGGAAGAACTTATGGATGCG

451
dms2c.pk005.c7 (SEQ ID NO:1) 500
ecslc.pk009.p19 (SEQ ID NO:3)
ehb2c.pk001.i10 (SEQ ID NO:5)

(349) AGAGCAGAGTGAAGCTGCTTCTGATGCGGCTTAACTGAAGTGATTT
(181) GCGGCTGCGGCTGCAATGCTGAGGCTGCTGAGAGCTGATGAGTTTAT
(274) AGGAACCTCATGAGCTGCTGAGAGCTGCTGAGAGCTGATGAGTTTAT

FIG. 2-4

6/24

ehb2c.pk001.d17 (SEQ ID NO:7)	(274) AGGAACCTCATGAGGTTCAAGGCTAATGCGATCTAAAGCTGGAGAGAT	(274) AGGAACCTCATGAGGTTCAAGGCTAATGCGATCTAAAGCTGGAGAGAT
ehb2c.pk001.o18 (SEQ ID NO:9)	(274) AGGAACCTCATGAGGTTCAAGGCTAATGCGATCTAAAGCTGGAGAGAT	(274) AGGAACCTCATGAGGTTCAAGGCTAATGCGATCTAAAGCTGGAGAGAT
r10n.pk117.i23 (SEQ ID NO:13)	(181) CAGATCCGACTGAGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT	(181) CAGATCCGACTGAGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT
rr1.pk005.h8 (SEQ ID NO:15)	(322) CAGATCCGACTGAGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT	(322) CAGATCCGACTGAGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT
sl1.pk0128.h7 (SEQ ID NO:17)	(445) CCGGCAAGCTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT	(445) CCGGCAAGCTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT
vdb1c.pk001.k23 (SEQ ID NO:11)	(415) CCGGCAAGCTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT	(415) CCGGCAAGCTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT
wdk5c.pk005.f22 (SEQ ID NO:19)	(271) CCGGCAAGCTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT	(271) CCGGCAAGCTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT
M.lutupps (SEQ ID NO:23)	(238) CCGGCAAGCTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT	(238) CCGGCAAGCTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT
yeast rer2 (SEQ ID NO:25)	(271) AGGAGCTCAGCGGAGGAGTACATGAGCTTGGCGGAGAGAT	(271) AGGAGCTCAGCGGAGGAGTACATGAGCTTGGCGGAGAGAT
yeast srl1 (SEQ ID NO:27)	(376) AGGAGCTCAGCGGAGGAGTACATGAGCTTGGCGGAGAGAT	(376) AGGAGCTCAGCGGAGGAGTACATGAGCTTGGCGGAGAGAT
dms2c.pk005.c7 (SEQ ID NO:1)	(399) AATGATGAGGTTTCTTCTTAAAGCTGGAGAGAT	(399) AATGATGAGGTTTCTTCTTAAAGCTGGAGAGAT
ecs1c.pk009.p19 (SEQ ID NO:3)	(231) GAGGACAGATGCTTAAAGCTGGAGAGAT	(231) GAGGACAGATGCTTAAAGCTGGAGAGAT
ehb2c.pk001.i10 (SEQ ID NO:5)	(324) TGAAGGAGGATC-----ATGGAAGAGTAAAGCTGGAGAGAT	(324) TGAAGGAGGATC-----ATGGAAGAGTAAAGCTGGAGAGAT
ehb2c.pk001.d17 (SEQ ID NO:7)	(324) TGAAGGAGGATC-----ATGGAAGAGTAAAGCTGGAGAGAT	(324) TGAAGGAGGATC-----ATGGAAGAGTAAAGCTGGAGAGAT
ehb2c.pk001.o18 (SEQ ID NO:9)	(324) TGAAGGAGGATC-----ATGGAAGAGTAAAGCTGGAGAGAT	(324) TGAAGGAGGATC-----ATGGAAGAGTAAAGCTGGAGAGAT
r10n.pk117.i23 (SEQ ID NO:13)	(231) CATTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT	(231) CATTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT
rr1.pk005.h8 (SEQ ID NO:15)	(372) CATTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT	(372) CATTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT
sl1.pk0128.h7 (SEQ ID NO:17)	(495) AATGATGAGGTTTCTTCTTAAAGCTGGAGAGAT	(495) AATGATGAGGTTTCTTCTTAAAGCTGGAGAGAT
vdb1c.pk001.k23 (SEQ ID NO:11)	(465) CATTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT	(465) CATTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT
wdk5c.pk005.f22 (SEQ ID NO:19)	(321) CATTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT	(321) CATTGAGGCTGAAATGTATGAGGCTTAAAGCTGGAGAGAT
M.lutupps (SEQ ID NO:23)	(288) AATGATGAGGTTTCTTCTTAAAGCTGGAGAGAT	(288) AATGATGAGGTTTCTTCTTAAAGCTGGAGAGAT
yeast rer2 (SEQ ID NO:25)	(321) ACGAGCTCAGCGGAGGAGTACATGAGCTTGGCGGAGAGAT	(321) ACGAGCTCAGCGGAGGAGTACATGAGCTTGGCGGAGAGAT
yeast srl1 (SEQ ID NO:27)	(426) TGAAGCTCAGCGGAGGAGTACATGAGCTTGGCGGAGAGAT	(426) TGAAGCTCAGCGGAGGAGTACATGAGCTTGGCGGAGAGAT
dms2c.pk005.c7 (SEQ ID NO:1)	(435) -CCAGCTTTCGGTTCGAGCTGAGCTGAGCTTAAAGCTGGAGAGAT	(435) -CCAGCTTTCGGTTCGAGCTGAGCTGAGCTTAAAGCTGGAGAGAT
ecs1c.pk009.p19 (SEQ ID NO:3)	(267) -CCAGCTTTCGGTTCGAGCTGAGCTGAGCTTAAAGCTGGAGAGAT	(267) -CCAGCTTTCGGTTCGAGCTGAGCTGAGCTTAAAGCTGGAGAGAT
ehb2c.pk001.i10 (SEQ ID NO:5)	(369) -CCAGCTTTCGGTTCGAGCTGAGCTTAAAGCTGGAGAGAT	(369) -CCAGCTTTCGGTTCGAGCTGAGCTTAAAGCTGGAGAGAT
ehb2c.pk001.d17 (SEQ ID NO:7)	(369) -CCAGCTTTCGGTTCGAGCTGAGCTTAAAGCTGGAGAGAT	(369) -CCAGCTTTCGGTTCGAGCTGAGCTTAAAGCTGGAGAGAT
ehb2c.pk001.o18 (SEQ ID NO:9)	(369) -CCAGCTTTCGGTTCGAGCTGAGCTTAAAGCTGGAGAGAT	(369) -CCAGCTTTCGGTTCGAGCTGAGCTTAAAGCTGGAGAGAT
r10n.pk117.i23 (SEQ ID NO:13)	(277) -AAATCTACATCTCG-GGAGCTTGGAGCTTAAAGCTGGAGAGAT	(277) -AAATCTACATCTCG-GGAGCTTGGAGCTTAAAGCTGGAGAGAT
rr1.pk005.h8 (SEQ ID NO:15)	(418) -AAATCTACATCTCG-GGAGCTTGGAGCTTAAAGCTGGAGAGAT	(418) -AAATCTACATCTCG-GGAGCTTGGAGCTTAAAGCTGGAGAGAT
sl1.pk0128.h7 (SEQ ID NO:17)	(531) -AAATCTACATCTCG-GGAGCTTGGAGCTTAAAGCTGGAGAGAT	(531) -AAATCTACATCTCG-GGAGCTTGGAGCTTAAAGCTGGAGAGAT
vdb1c.pk001.k23 (SEQ ID NO:11)	(500) -CCAGCTTTCGGTTCGAGCTGAGCTTAAAGCTGGAGAGAT	(500) -CCAGCTTTCGGTTCGAGCTGAGCTTAAAGCTGGAGAGAT
wdk5c.pk005.f22 (SEQ ID NO:19)	(357) -CCAGCTTTCGGTTCGAGCTGAGCTTAAAGCTGGAGAGAT	(357) -CCAGCTTTCGGTTCGAGCTGAGCTTAAAGCTGGAGAGAT

FIG. 2-5

7/24

M. lutupps	(SEQ ID NO:23)	(324)	-TAACTGAAACGATTTGGCTTTATGTGATGATTTACCGGACCATACATCA
yeast rer2	(SEQ ID NO:25)	(365)	TACCAATAAAATATCCGCGATCTCTTTGTTGGATATCTTCATTT
yeast srl1	(SEQ ID NO:27)	(476)	CTAAATAGAAATAGTACGGTGTCAATTTTACATCTCCAGAAAGGG
dms2c.pk005.c7	(SEQ ID NO:1)	601	CGGATCATTACATTTCTCTTAATCTCGAGAGAACCTGACATCTCA
ecs1c.pk009.p19	(SEQ ID NO:3)	(484)	TAGTTTCATCGAAATAGAGAAATCAAGAGCCATTTAGAGACCCA
ehb2c.pk001.i10	(SEQ ID NO:5)	(418)	ACCGAGCAGATAGATATAGGGGTATGTGCCATCATTTCCAAATGTGT
ehb2c.pk001.d17	(SEQ ID NO:7)	(418)	ACCGAGCAGATAGATATAGGGGTATGTGCCATCATTTCCAAATGTGT
ehb2c.pk001.o18	(SEQ ID NO:9)	(418)	ATCGAGCAGAAAGATATAGGGGTATGTGCCATCATTTCCGGCTTGT
r10n.pk117.i23	(SEQ ID NO:13)	(325)	GTAGAGCTGAGTAACATGATGGCTACCTGTCTGAATACAGGGACGGT
rr1.pk005.h8	(SEQ ID NO:15)	(466)	GTAGAGCTGAGTAACATGATGGCTACCTGTCTGAATACAGGGACGGT
s11.pk0128.h7	(SEQ ID NO:17)	(580)	GAATGATAGCTTGTTCAGTAAGATTAACAAATATTTGAGATTTCCA
vdbl.c.pk001.k23	(SEQ ID NO:11)	(547)	CTGAT---AATTGTTTACAGGAGCTCTTAGGAGTCTTGGCAATACA
wdk5c.pk005.f22	(SEQ ID NO:19)	(406)	TAGATTCACGAGTCCCTAGGAGCTCTTAGGAGTCTTGGCAATACA
M. lutupps	(SEQ ID NO:23)	(373)	TAAAGATGTTAGTACCGTAAGGAAATCTGAACATTTTACCTTTAAC
yeast rer2	(SEQ ID NO:25)	(415)	GAAATTTTCGGGTCTCTGTAAGTCTGTAAGATCTCAAAAGGGCCAC
yeast srl1	(SEQ ID NO:27)	(526)	TAAATATTAATAGTGGAAATCTACAGGTTGGAGACGATTTTAC
dms2c.pk005.c7	(SEQ ID NO:1)	651	TGTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
ecs1c.pk009.p19	(SEQ ID NO:3)	(366)	TGTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
ehb2c.pk001.i10	(SEQ ID NO:5)	(468)	GTTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
ehb2c.pk001.d17	(SEQ ID NO:7)	(468)	GTTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
ehb2c.pk001.o18	(SEQ ID NO:9)	(468)	GTTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
r10n.pk117.i23	(SEQ ID NO:13)	(375)	-TGTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
rr1.pk005.h8	(SEQ ID NO:15)	(516)	-TGTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
s11.pk0128.h7	(SEQ ID NO:17)	(630)	AGTTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
vdbl.c.pk001.k23	(SEQ ID NO:11)	(594)	GTTCATTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
wdk5c.pk005.f22	(SEQ ID NO:19)	(456)	TGTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
M. lutupps	(SEQ ID NO:23)	(423)	GTTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
yeast rer2	(SEQ ID NO:25)	(465)	GTTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
yeast srl1	(SEQ ID NO:27)	(576)	TTTATATATGTTTCTCTTACCTTACCTTACCTTACCTTACCTTACCTTAC
dms2c.pk005.c7	(SEQ ID NO:1)	700	TGTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
ecs1c.pk009.p19	(SEQ ID NO:3)	(366)	TGTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
ehb2c.pk001.i10	(SEQ ID NO:5)	(468)	GTTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
ehb2c.pk001.d17	(SEQ ID NO:7)	(468)	GTTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
ehb2c.pk001.o18	(SEQ ID NO:9)	(468)	GTTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
r10n.pk117.i23	(SEQ ID NO:13)	(375)	-TGTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
rr1.pk005.h8	(SEQ ID NO:15)	(516)	-TGTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
s11.pk0128.h7	(SEQ ID NO:17)	(630)	AGTTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
vdbl.c.pk001.k23	(SEQ ID NO:11)	(594)	GTTCATTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
wdk5c.pk005.f22	(SEQ ID NO:19)	(456)	TGTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
M. lutupps	(SEQ ID NO:23)	(423)	GTTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
yeast rer2	(SEQ ID NO:25)	(465)	GTTTCGTCAGCAATAAATATATGCT--GCATAATATGATATCTCCATAC
yeast srl1	(SEQ ID NO:27)	(576)	TTTATATATGTTTCTCTTACCTTACCTTACCTTACCTTACCTTACCTTAC

FIG. 2-6

8/24

FIG. 2-7

dms2c.pk005.c7	(SEQ ID NO:1)	701	TTCTCAAGCATGGGACTA	750
ecslc.pk009.p19	(SEQ ID NO:3)	(582)	TTCTCAAGCATGGGACTA	
ehb2c.pk001.i10	(SEQ ID NO:5)	(414)	TTCTCAAGCATGGGACTA	
ehb2c.pk001.d17	(SEQ ID NO:7)	(516)	TTGAACTCCAAATGAAGTTTGTAAACA	
ehb2c.pk001.o18	(SEQ ID NO:9)	(516)	TTGAACTCCAAATGAAGTTTGTAAACA	
r10n.pk117.i23	(SEQ ID NO:13)	(516)	TTGAACTCCAAATGAAGTTTGTAAACA	
rr1.pk005.h8	(SEQ ID NO:15)	(423)	GGTCAATTAAGGTCGTGCA	---ATA
s11.pk0128.h7	(SEQ ID NO:17)	(564)	GGTCAATTAAGGTCGTGCA	---ATA
vdb1c.pk001.k23	(SEQ ID NO:11)	(678)	ATCAATTAAGGTCGTGCA	
wdk5c.pk005.f22	(SEQ ID NO:19)	(642)	ATCAATTAAGGTCGTGCA	
M.lutupps	(SEQ ID NO:23)	(504)	ATGCCGATTCGCGCCG	
yeast rer2	(SEQ ID NO:25)	(471)	AGCGGTTAAAGGTCGTGCA	
yeast srt1	(SEQ ID NO:27)	(513)	CAATTAAGGTCGTGCA	
		(624)	TATTCGTGTTCAATTAAGGTCGTGCA	

dms2c.pk005.c7	(SEQ ID NO:1)	751	TTGCAAGCATGGGACTA	800
ecslc.pk009.p19	(SEQ ID NO:3)	(601)	TTGCAAGCATGGGACTA	
ehb2c.pk001.i10	(SEQ ID NO:5)	(433)	TTGCAAGCATGGGACTA	
ehb2c.pk001.d17	(SEQ ID NO:7)	(560)	CAAGATTAAGGTCGTGCA	
ehb2c.pk001.o18	(SEQ ID NO:9)	(560)	CAAGATTAAGGTCGTGCA	
r10n.pk117.i23	(SEQ ID NO:13)	(566)	ATGGGATTGAAGTCGTGCA	
rr1.pk005.h8	(SEQ ID NO:15)	(457)	CTGCAGGTCGTGCA	---GA
s11.pk0128.h7	(SEQ ID NO:17)	(598)	CTGCAGGTCGTGCA	---GA
vdb1c.pk001.k23	(SEQ ID NO:11)	(697)	ATCAATTAAGGTCGTGCA	
wdk5c.pk005.f22	(SEQ ID NO:19)	(661)	ATCAATTAAGGTCGTGCA	
M.lutupps	(SEQ ID NO:23)	(523)	ATCAATTAAGGTCGTGCA	
yeast rer2	(SEQ ID NO:25)	(490)	GTTACAATCTG	
yeast srt1	(SEQ ID NO:27)	(557)	ACGAAAGCAGCTTACGTCGTGCA	
		(674)	ATATAAGAAATTTACATAATTAAGGTCGTGCA	

dms2c.pk005.c7	(SEQ ID NO:1)	801	TTGCAAGCATGGGACTA	850
ecslc.pk009.p19	(SEQ ID NO:3)	(616)	TTGCAAGCATGGGACTA	
ehb2c.pk001.i10	(SEQ ID NO:5)	(448)	TTGCAAGCATGGGACTA	
ehb2c.pk001.d17	(SEQ ID NO:7)	(595)	AGTACTGTCGTGCA	
ehb2c.pk001.o18	(SEQ ID NO:9)	(595)	AGTACTGTCGTGCA	
		(616)	AGTACTGTCGTGCA	

FIG. 2-8

		901			950
dms2c.pk005.c7	(SEQ ID NO:1)	(702)	AAATTGGCGTAGAGTGGGAGCTTAAGAGGAGGAGCTTCTTTTGTGCTGCTAT		
ecs1c.pk009.p19	(SEQ ID NO:3)	(534)	TATAAGCTTAGAGCGGGATATAGGCTTAGCTATTTCAAGGCTTGGCTGTA		
ehb2c.pk001.i10	(SEQ ID NO:5)	(693)	CAATTGCAAGATCTGGGAGATCCCTTTGACGAGCTACTTAAGTTTGGCAAA		
ehb2c.pk001.d17	(SEQ ID NO:7)	(693)	CAATTGCAAGATCTGGGAGATCCCTTTGACGAGCTACTTAAGTTTGGCAAA		
ehb2c.pk001.o18	(SEQ ID NO:9)	(711)	CAATTGCAAGATCTGGGTTTGGCTTGTAAAGCTTGTCACTAAGTTTGGCAAA		
rl0n.pk117.i23	(SEQ ID NO:13)	(570)	CAATCCGATGCTCAGGTGATATGCTCCATGACGATTTCTCTTGTGTTGGCAAA		
rrl.pk005.h8	(SEQ ID NO:15)	(711)	CAATCCGATGCTCAGGTGATATGCTCCATGACGATTTCTCTTGTGTTGGCAAA		
sl1.pk0128.h7	(SEQ ID NO:17)	(798)	AAATAGATATAGTGGCTACTTAAGAGTCACTAGCTTGTGTTGGCAAA		
vdb1c.pk001.k23	(SEQ ID NO:11)	(762)	TATAGCAATAGATGGCTACTTAAGAGTCACTAGCTTGTGTTGGCAAA		
wdk5c.pk005.f22	(SEQ ID NO:19)	(618)	CTATCAGTGGCAGCGGCCACTGAGGCTGAGGAGCTTCCGCTGATAGTGGCAAT		
M.lutups	(SEQ ID NO:23)	(585)	AAATCAGAAATCCGGTGAAGAACGTTTAAAGTATTTTAAATTGGCAAT		

10/24

yeast rer2 (SEQ ID NO:25)	(696)	GATTCT--ATATGGCCAGAGCT-----TTGGATCTATACGG-ATGGATG
yeast srl1 (SEQ ID NO:27)	(814)	GATAGC-----ATGGCCCAATAT-----TTACCTTTTGCTATGATACCTGA
dms2c.pk005.c7 (SEQ ID NO:1)	951	TGGCGATATCTGATTTATATCTTCAGAGAAAGTCTTTGGGCTCATTTTTCG
ecs1c.pk009.p19 (SEQ ID NO:3)	(752)	TGGCGATATCTGATTTATATCTTCAGAGAAAGTCTTTGGGCTCATTTTTCG
ehb2c.pk001.i10 (SEQ ID NO:5)	(584)	TGGCGATATCTGATTTATATCTTCAGAGAAAGTCTTTGGGCTCATTTTTCG
ehb2c.pk001.d17 (SEQ ID NO:7)	(743)	CTAGTAATTCATAGCTGTTCTTCCTATGACGCTGGGAGAGATTCG
ehb2c.pk001.o18 (SEQ ID NO:9)	(743)	CTAGTAATTCATAGCTGTTCTTCCTATGACGCTGGGAGAGATTCG
rl0n.pk117.i23 (SEQ ID NO:13)	(761)	CTAGTAATTCATAGCTGTTCTTCCTATGACGCTGGGAGAGATTCG
rr1.pk005.h8 (SEQ ID NO:15)	(620)	CGAGGTCAGTCTTTTCAGAAACAGACCTCTTTTGGGCTCATTTTTCG
s11.pk0128.h7 (SEQ ID NO:17)	(761)	CGAGGTCAGTCTTTTCAGAAACAGACCTCTTTTGGGCTCATTTTTCG
vdb1c.pk001.k23 (SEQ ID NO:19)	(848)	TAGGCTATCTGAGCTTTTTCAGAAACAGACCTCTTTTGGGCTCATTTTTCG
wdk5c.pk005.f22 (SEQ ID NO:23)	(812)	TAGGCTATCTGAGCTTTTTCAGAAACAGACCTCTTTTGGGCTCATTTTTCG
M.lutupps (SEQ ID NO:25)	(668)	CGGCTATCTGAGCTTTTTCAGAAACAGACCTCTTTTGGGCTCATTTTTCG
yeast rer2 (SEQ ID NO:25)	(635)	GTTTATATAGTGTGTGTATATAGTGTGTGTATATAGTGTGTGTATATAGT
yeast srl1 (SEQ ID NO:27)	(738)	GATTAT
	(857)	TG-----ATCTCTATATGGTCTCTTTTCCACGATTTTAAAAATATATAT
dms2c.pk005.c7 (SEQ ID NO:1)	1001	GGAGTGTACCTTTACATGCTTTTATATACTTTTCAATATAGAGAGAGAGAG
ecs1c.pk009.p19 (SEQ ID NO:3)	(802)	GGAGTGTACCTTTACATGCTTTTATATACTTTTCAATATAGAGAGAGAGAG
ehb2c.pk001.i10 (SEQ ID NO:5)	(634)	GGAGTGTACCTTTACATGCTTTTATATACTTTTCAATATAGAGAGAGAGAG
ehb2c.pk001.d17 (SEQ ID NO:7)	(793)	CTTCGACCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
ehb2c.pk001.o18 (SEQ ID NO:9)	(793)	CTTCGACCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
rl0n.pk117.i23 (SEQ ID NO:13)	(811)	CTCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
rr1.pk005.h8 (SEQ ID NO:15)	(670)	TTCAAGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
s11.pk0128.h7 (SEQ ID NO:17)	(811)	TTCAAGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
vdb1c.pk001.k23 (SEQ ID NO:19)	(898)	ATGGTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
wdk5c.pk005.f22 (SEQ ID NO:23)	(862)	ATGGTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
M.lutupps (SEQ ID NO:25)	(718)	GGGGCCAT
yeast rer2 (SEQ ID NO:25)	(685)	GGAGTAAGTTTTCACATATATATATATATATATATATATATATATATATATAT
yeast srl1 (SEQ ID NO:27)	(788)	GTTTGGAGGAGCTTTGATTATGTCGAGGAAAGGATTTGGGAGCCCCATCG
	(901)	GGAGTGTACCTTTACATGCTTTTATATACTTTTCAATATAGAGAGAGAGAG
dms2c.pk005.c7 (SEQ ID NO:1)	1051	TTATGGTGTGATG-----
	1100	

FIG. 2-9

12/24

1 50
 (1) --MLNPLYLKYP-----CYFPASLSTNNHHRGLYVF
 (1) -----
 (1) -----MELYNG
 (1) -----MELYNG
 (1) -----MEITYG
 (1) MLSEFRFPIADNARHTFKSHSSCTFRSNRIDSFSFPPISVPRFHKLRTA
 (1) -----
 (1) -----MLGSLMSYLPVSDSKTENTDEL
 (1) -----
 (1) MFSRLRLPIPLVKTPSPSCYYSHYHYRYRCYHPFHRSQTQSLIVSK
 (1) -----
 (1) -----MPLSN

dms2c.pk005.c7 (SEQ ID NO:2)
 ecs1c.pk009.p19 (SEQ ID NO:4)
 ehb2c.pk001.i10 (SEQ ID NO:6)
 ehb2c.pk001.d17 (SEQ ID NO:8)
 ehb2c.pk001.o18 (SEQ ID NO:10)
 vdb1c.pk001.k23 (SEQ ID NO:12)
 r10n.pk117.i23 (SEQ ID NO:14)
 rrl1.pk0050.h8 (SEQ ID NO:16)
 sl1.pk0128.h7 (SEQ ID NO:18)
 wdk5c.pk005.f22 (SEQ ID NO:20)

51 100
 (31) NQSDTTGGGINSLEERIT-----PAGKHHELPKHHVAVLMDGN
 (1) -----MPKHVAVLMDGN
 (7) ERPSVFRLLGKYMKGKLY-----STTQGPPIPTHIAVLDGN
 (7) ERPSVFRLLGKYMKGKLY-----STTQGPPIPTHIAVLDGN
 (7) QRPSPFRIFGKYMKGKLY-----STTQGPPIPTHIAVLDGN
 (51) KTDVVGEEEAAREVNERAEFF-----PDGRRRLVPEHVAVLDGN
 (1) -----MPKHVAVLMDGN
 (23) IATCGLASLQNFIRKCIV-----AVSYGPPKHHVAVLMDGN
 (51) RGSALAKCHADSVTLRDDGVSLAQESLEPLPAEPAEMVPKHHVAVLMDGN
 (6) STSSPAVTVPAAEELLS-----QGRRAESLPRHVALVLDGN

dms2c.pk005.c7 (SEQ ID NO:2)
 ecs1c.pk009.p19 (SEQ ID NO:4)
 ehb2c.pk001.i10 (SEQ ID NO:6)
 ehb2c.pk001.d17 (SEQ ID NO:8)
 ehb2c.pk001.o18 (SEQ ID NO:10)
 vdb1c.pk001.k23 (SEQ ID NO:12)
 r10n.pk117.i23 (SEQ ID NO:14)
 rrl1.pk0050.h8 (SEQ ID NO:16)
 sl1.pk0128.h7 (SEQ ID NO:18)
 wdk5c.pk005.f22 (SEQ ID NO:20)

101 150
 (69) RRMARSGCTMPDAGYMEARS[KVMVELGRKW]IQVLAIFA[FSAD]NLAP
 (13) RRMAREKQSPMT[HS]MRKT[QSL]FRQSKFKI[AVSI]KAFESTENWTRP
 (44) RRFARKKH[GG]KAGFLAL[LVN]VTVGVLEV[Q]AI[VA]FSIDNFRK
 (44) RRFARKKH[GG]KAGFLAL[LVN]VTVGVLEV[Q]AI[VA]FSIDNFRK
 (44) RRFARKKH[GG]KAGFLAL[LVN]VTVGVLEV[Q]AI[VA]FSIDNFRK
 (91) VRMDOKR[GG]AAS[Q]QAGVRS[REL]VELCKWE[IVLS]FA[FSYD]WSFS
 (13) RRYAF[FS]IQ[GS]CHRV[FS]IASL[GV]MEV[VA]I[VA]FSIDNFKD
 (60) RRYAF[FS]IQ[GS]CHRV[FS]IASL[GV]MEV[VA]I[VA]FSIDNFKD

dms2c.pk005.c7 (SEQ ID NO:2)
 ecs1c.pk009.p19 (SEQ ID NO:4)
 ehb2c.pk001.i10 (SEQ ID NO:6)
 ehb2c.pk001.d17 (SEQ ID NO:8)
 ehb2c.pk001.o18 (SEQ ID NO:10)
 vdb1c.pk001.k23 (SEQ ID NO:12)
 r10n.pk117.i23 (SEQ ID NO:14)
 rrl1.pk0050.h8 (SEQ ID NO:16)

FIG. 3-1

13/24

s11.pk0128.h7 (SEQ ID NO:18)	(101)	G	A	K	U	P	S	A	C	H	Q	A	G	V	Q	S	R	K	M	V	R	L	C	S	W	G	I	A	V	L	A	F	A	S	T	E	N	N	V	P
wdk5c.pk005.f22 (SEQ ID NO:20)	(43)	S	A	A	R	C	H	P	T	D	C	H	M	R	A	M	R	T	V	R	L	S	R	A	W	I	R	V	L	A	F	G	S	L	E	N	N	P		
dms2c.pk005.c7 (SEQ ID NO:2)	(119)	K	V	E	D	T	G	I	S	V	L	K	D	E	V	V	H	M	I	K	E	---	Q	I	L	S	V	I	D	T	S	K	P	K	S	K	R	I	T	
ecs1c.pk009.p19 (SEQ ID NO:4)	(63)	K	E	V	D	T	G	I	S	V	L	K	D	E	V	V	H	M	I	K	E	---	C	R	V	S	I	M	K	K	T	N	P	K	S	L	O	K	L	C
ehb2c.pk001.i10 (SEQ ID NO:6)	(94)	H	E	V	Q	V	D	M	L	K	E	G	M	I	M	E	S	I	I	N	A	Y	D	I	C	V	R	F	V	E	N	K	L	S	E	P	K	T	A	
ehb2c.pk001.d17 (SEQ ID NO:8)	(94)	H	E	V	Q	V	D	M	L	K	E	G	M	I	M	E	S	I	I	N	A	Y	D	I	C	V	R	F	V	E	N	K	L	S	E	P	K	T	A	
ehb2c.pk001.o18 (SEQ ID NO:10)	(94)	H	E	V	Q	V	D	M	L	K	E	G	M	I	M	E	S	I	I	N	A	Y	D	I	C	V	R	F	V	E	N	K	L	S	E	P	K	T	A	
rdb1c.pk001.k23 (SEQ ID NO:12)	(141)	E	G	V	G	E	H	S	H	I	R	V	V	A	E	P	I	L	G	---	E	K	A	F	E	C	R	D	W	G	F	V	K	A	S	E	Q	L	O	
r10n.pk117.i23 (SEQ ID NO:14)	(63)	H	T	V	K	S	E	M	E	E	K	N	E	L	L	E	N	R	N	V	I	N	K	V	N	C	K	I	N	F	W	E	N	D	M	I	S	K	S	
rr1.pk0050.h8 (SEQ ID NO:16)	(110)	H	T	V	K	S	E	M	E	E	K	N	E	L	L	E	N	R	N	V	I	N	K	V	N	C	K	I	N	F	W	E	N	D	M	I	S	K		
s11.pk0128.h7 (SEQ ID NO:18)	(151)	K	V	E	D	T	G	I	S	V	L	K	D	E	V	V	H	M	I	K	E	---	G	I	R	S	V	I	D	S	S	R	P	E	S	L	K			
wdk5c.pk005.f22 (SEQ ID NO:20)	(93)	K	A	E	D	T	G	I	S	V	L	K	D	E	V	V	H	M	I	K	E	---	E	T	R	L	R	I	I	E	D	R	S	R	P	I	S			
dms2c.pk005.c7 (SEQ ID NO:2)	(166)	Y	A	E	N	I	K	N	S	O	I	N	E	V	A	I	N	E	G	K	Y	D	I	O	Q	S	I	A	L	K	D	G	V	I	O	P	E			
ecs1c.pk009.p19 (SEQ ID NO:4)	(110)	E	I	E	K	S	R	A	N	G	T	H	V	N	I	N	E	G	K	Y	D	I	E	A	C	K	S	V	A	T	K	D	G	V	I	I	P			
ehb2c.pk001.i10 (SEQ ID NO:6)	(144)	K	I	M	R	A	N	N	K	C	M	L	L	I	V	C	T	S	D	E	H	A	V	E	S	---	E	L	N	S	E	V	C	N	---	---	---			
ehb2c.pk001.d17 (SEQ ID NO:8)	(144)	K	I	M	R	A	N	N	K	C	M	L	L	I	V	C	T	S	D	E	H	A	V	E	S	---	E	L	N	S	E	V	C	N	---	---	---			
ehb2c.pk001.o18 (SEQ ID NO:10)	(144)	K	I	M	R	A	N	N	K	C	M	L	L	I	V	C	T	S	D	E	H	A	V	E	S	---	E	L	N	S	E	V	C	N	---	---	---			
vdb1c.pk001.k23 (SEQ ID NO:12)	(186)	D	V	E	E	T	K	E	N	S	R	O	F	I	A	L	S	I	S	G	O	C	D	L	O	A	C	K	N	I	G	H	K	D	G	L				
r10n.pk117.i23 (SEQ ID NO:14)	(113)	K	L	M	A	T	A	E	N	T	G	F	S	C	M	P	N	S	I	S	E	L	N	A	N	V	N	K	V	C	---	---	---	---	---	---				
rr1.pk0050.h8 (SEQ ID NO:16)	(160)	K	L	M	A	T	A	E	N	T	G	F	S	C	M	P	N	S	I	S	E	L	N	A	N	V	N	K	V	C	---	---	---	---	---	---				
s11.pk0128.h7 (SEQ ID NO:18)	(198)	S	A	E	E	D	K	O	N	S	R	F	O	I	A	L	S	I	S	G	K	Y	D	I	O	Q	C	K	S	V	A	K	K	D	G					
wdk5c.pk005.f22 (SEQ ID NO:20)	(140)	D	A	E	A	I	R	N	S	O	I	N	E	V	A	I	N	E	G	K	Y	D	I	O	Q	S	I	A	L	K	D	G	V	I	I	P				
dms2c.pk005.c7 (SEQ ID NO:2)	(212)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
ecs1c.pk009.p19 (SEQ ID NO:4)	(156)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---					
ehb2c.pk001.i10 (SEQ ID NO:6)	(188)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---					
ehb2c.pk001.d17 (SEQ ID NO:8)	(188)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---					
ehb2c.pk001.o18 (SEQ ID NO:10)	(194)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---					
vdb1c.pk001.k23 (SEQ ID NO:12)	(232)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---					
r10n.pk117.i23 (SEQ ID NO:14)	(150)	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---					

FIG. 3-2

14/24

rrl.pk0050.h8 (SEQ ID NO:16) ---R---DILQREDADSVANNGVSDISVAIDDRHNVSAGCDPDIVIRI
 sl1.pk0128.h7 (SEQ ID NO:18) -----INENIEQDEENCTEFYDPDIIIRI
 wdk5c.pk005.f22 (SEQ ID NO:20) -----IDESIFADIIQI--SETSCPDIIRI

301 (238) SGLRVSNIETWOLAYTELISESETIETDEDEELHINTQHRRRYGG 350
 (182) SGLRVSNIETWOLAYTELISESETIETDEDEELHINTQHRRRYGG
 (235) SGLRVSNIETWOLAYTELISESETIETDEDEELHINTQHRRRYGG
 (235) SGLRVSNIETWOLAYTELISESETIETDEDEELHINTQHRRRYGG
 (241) SGLRVSNIETWOLAYTELISESETIETDEDEELHINTQHRRRYGG
 (258) SGLRVSNIETWOLAYTELISESETIETDEDEELHINTQHRRRYGG
 (194) SGLRVSNIETWOLAYTELISESETIETDEDEELHINTQHRRRYGG
 (241) SGLRVSNIETWOLAYTELISESETIETDEDEELHINTQHRRRYGG
 (270) SGLRVSNIETWOLAYTELISESETIETDEDEELHINTQHRRRYGG
 (210) SGLRVSNIETWOLAYTELISESETIETDEDEELHINTQHRRRYGG

351 (288) dms2c.pk005.c7 (SEQ ID NO:2) -----
 (229) ecs1c.pk009.p19 (SEQ ID NO:4) -----
 (285) ehb2c.pk001.i10 (SEQ ID NO:6) HKEYLA
 (285) ehb2c.pk001.d17 (SEQ ID NO:8) HKEYLA
 (291) ehb2c.pk001.o18 (SEQ ID NO:10) HKEYLA
 (308) vdb1c.pk001.k23 (SEQ ID NO:12) RN
 (244) r10n.pk117.i23 (SEQ ID NO:14) SRNLAKQL
 (291) rrl.pk0050.h8 (SEQ ID NO:16) SRNLAKQL
 (320) sl1.pk0128.h7 (SEQ ID NO:18) RHS
 (260) wdk5c.pk005.f22 (SEQ ID NO:20) RKNNAL--

FIG. 3-3

15/24

1 50

M.lutUPPS (SEQ ID NO:24) -----

Yeaststr1 (SEQ ID NO:28) -----MKMPSIIQIQFVALKRLLVETKEQMCF

Yeastrer2 (SEQ ID NO:26) -----METDSGIP

dms2c.pk005.c7 (SEQ ID NO:2) -----CYFPASLSTNHHRGLYVF

ecs1c.pk009.p19 (SEQ ID NO:4) -----

ehb2c.pk001.i10 (SEQ ID NO:6) -----MELNG

ehb2c.pk001.d17 (SEQ ID NO:8) -----MELNG

ehb2c.pk001.o18 (SEQ ID NO:10) -----MEIYTG

vdb1c.pk001.k23 (SEQ ID NO:12) -----

r10n.pk117.i23 (SEQ ID NO:14) -----

rr1.pk0050.h8 (SEQ ID NO:16) -----MLGSLMSYLPVSDKTENTDEL

s11.pk0128.h7 (SEQ ID NO:18) -----MFSLRPLPLVKTPPSPSCYSHYHYRYRCYHPFHRSQTQSLIVSK

wdk5c.pk005.f22 (SEQ ID NO:20) -----MPLSN

FIG. 4-1

51 100

M.lutUPPS (SEQ ID NO:24) -----

Yeaststr1 (SEQ ID NO:28) -----INAAQIEKHIAIIMDGN

Yeastrer2 (SEQ ID NO:26) -----AVKSIQFVFAWMSLSLFSWFYNLQNILIKARVGPVEHIVSEIMDGN

dms2c.pk005.c7 (SEQ ID NO:2) -----GHSFVWKTKNIFSRITLR-----ASNCVFRIMGEMDGN

ecs1c.pk009.p19 (SEQ ID NO:4) -----NQSDTTGGGINSLEERIT-----PAGEKHELMKHAIVIMDGN

ehb2c.pk001.i10 (SEQ ID NO:6) -----ERPSVFRLLGKYMKGKLY-----SIITQGPITTHIIMDGN

ehb2c.pk001.d17 (SEQ ID NO:8) -----ERPSVFRLLGKYMKGKLY-----SIITQGPITTHIIMDGN

ehb2c.pk001.o18 (SEQ ID NO:10) -----QRPSVFRIFGKYMKGKLY-----SIITQGPITTHIIMDGN

vdb1c.pk001.k23 (SEQ ID NO:12) -----KTDVVGEEAEAREVNERAEF-----PDGIRRELMEHIVIMDGN

r10n.pk117.i23 (SEQ ID NO:14) -----IATGVLASLQNFIRKIV-----AVSYGPMKHAIAIMDGN

rr1.pk0050.h8 (SEQ ID NO:16) -----RGSIAKACHADSVTLRDDGVSLAQESLEPLPAEIAAEMMKHAIVIMDGN

s11.pk0128.h7 (SEQ ID NO:18) -----STSSVPAVTVPAEELLS-----QGRAESLPRHIVIMDGN

wdk5c.pk005.f22 (SEQ ID NO:20) -----

101 150

M.lutUPPS (SEQ ID NO:24) -----

(32) GRWAKQKKNRIKGIYEEMQTVKKITRYASDLGVKYLIVAEESTENWSPR

16/24

FIG. 4-2

SUBSTITUTE SHEET (RULE 26)

Yeaststr1 (SEQ ID NO:28)
 Yeastrer2 (SEQ ID NO:26)
 dms2c.pk005.c7 (SEQ ID NO:2)
 ecs1c.pk009.p19 (SEQ ID NO:4)
 ehb2c.pk001.i10 (SEQ ID NO:6)
 ehb2c.pk001.d17 (SEQ ID NO:8)
 ehb2c.pk001.o18 (SEQ ID NO:10)
 vdb1c.pk001.k23 (SEQ ID NO:12)
 r10n.pk117.i23 (SEQ ID NO:14)
 rr1.pk0050.h8 (SEQ ID NO:16)
 sl1.pk0128.h7 (SEQ ID NO:18)
 wdk5c.pk005.f22 (SEQ ID NO:20)

(78) RRYAKSRPVEVKKGEAGGLTTLTYIKRLGVKCVSAESENRRP
 (43) RRFARKKENDVKEGEAGFVMSRIHELVEAGVDTAVFAESENKRS
 (69) RRFARSRCMPDAGMEARSKVMVELRKWGIQVLFVESADNWLRP
 (13) RRFAVEKGSMPGCSMRKTQSLFRGSKFKIAVSIWSTENWTRP
 (44) RRFARKKHMEGGCKKCFLLNVITYYELGVYAYIAFSDNRRK
 (44) RRFARKKHMEGGCKKCFLLNVITYYELGVYAYIAFSDNRRK
 (44) RRFARKKHMEGGCKKCFLLNVITYYELGVYAYIAFSDNRRK
 (91) VFWAQKRCGHAASCHQAGVRSRELVELCKWGIKLVSAFSPYNSRS
 (13) RRYAFRSIOEGSCHRVFSAIASLYGYEMGVYIIVNAFSDNRRK
 (60) RRYAFRSIOEGSCHRVFSAIASLYGYEMGVYIIVNAFSDNRRK
 (101) GRWAKVKGHPGACQAGVQSIRKMVRLCSWGIKLVNAFSDNRRP
 (43) SRWAAARGGPTDCEHEMRALMRTVRLSRAGIRVLAFGFSELENRRP

151

M.lutUPPS (SEQ ID NO:24)
 Yeaststr1 (SEQ ID NO:28)
 Yeastrer2 (SEQ ID NO:26)
 dms2c.pk005.c7 (SEQ ID NO:2)
 ecs1c.pk009.p19 (SEQ ID NO:4)
 ehb2c.pk001.i10 (SEQ ID NO:6)
 ehb2c.pk001.d17 (SEQ ID NO:8)
 ehb2c.pk001.o18 (SEQ ID NO:10)
 vdb1c.pk001.k23 (SEQ ID NO:12)
 r10n.pk117.i23 (SEQ ID NO:14)
 rr1.pk0050.h8 (SEQ ID NO:16)
 sl1.pk0128.h7 (SEQ ID NO:18)
 wdk5c.pk005.f22 (SEQ ID NO:20)

(82) KDEVNYTKKPGDFLNTFLPELIEKN-----VKVETIGFIDDPDHTKKA
 (128) KEVDTHNNFTVKLDEFKAKRDKDLYGSKIRIVDQSLSPEMRKK
 (93) SREVESMTARERROITERGELACK--YGVRIKIIDLSIDKSLLED
 (119) KVEVDFMGIIISVLKDEVVHMIKE-----GIQLSVIGDTSKPKGVKRI
 (63) KEVDFTMEMYDILRTDAEELLSL-----GCRVSIMKKTNPGLQKL
 (94) PHEVQYVMDMLEKEGMEEMEEIINA--YDICRVFVGNLKLSEPVKTA
 (94) PHEVQYVMDMLEKEGMEEMEEIINA--YDICRVFVGNLKLSEPVKTA
 (94) PREVQVNMNMEKEEIIVEESIMNA--YDVGVRIVGNLNLDEPIRIA
 (141) EGEVGFVMSIIRVVKAELPILG-----GKAFECRDWGFVKASEQLQL
 (63) PTEVKSMEEMKEKNELLENRNVIN--VNCKINFWGNLDMSKSVRVA
 (110) PTEVKSMEEMKEKNELLENRNVIN--VNCKINFWGNLDMSKSVRVA
 (151) KVEVDFTMRFTNSENSEVQTFKRE-----GIRISVIGDSSRPESLKR
 (93) KAEVDFTMAIIRFINDNLAEFLRE-----GTRLRIGDRSRPIGVQKT

250

M.lutUPPS (SEQ ID NO:24)
 Yeaststr1 (SEQ ID NO:28)
 Yeastrer2 (SEQ ID NO:26)
 dms2c.pk005.c7 (SEQ ID NO:2)
 ecs1c.pk009.p19 (SEQ ID NO:4)
 ehb2c.pk001.i10 (SEQ ID NO:6)
 ehb2c.pk001.d17 (SEQ ID NO:8)
 ehb2c.pk001.o18 (SEQ ID NO:10)

(127) VLEAKKIKKHNTGLTAVFNLNGGRKEIISVQLIAERYKSGEISLDE--
 (178) IKKVEIIGDGDFTICFPYTSRNDMLHTIRDSVEDHLEN---KSP-
 (141) VRVAVTGNKIKRATINICFPYTGREELHLHMKETIVQHKGAIDES--
 (164) IITYAENIKNNSQLNIVVAINISGKYDVOQCOSIALKVKDGVIOPEE--
 (108) CIEIEKSRANSQTHVYALNLSGKYDIIECKSVATKVKDGVIIPKQ--
 (142) ADKIMRAJANNKCVLLTAVCTSTDEIYHVAVEESS--ELNSNEVCNN--
 (142) ADKIMRAJANNKCVLLTAVCTSTDEIYHVAVEESS--ELNSNEVCNN--
 (142) AEKIMRAJANNKGVLLTAVASSTDEIYHVAVEESSKDKLNSNEVCNNGI

17/24

FIG. 4-3

SUBSTITUTE SHEET (RULE 26)

vdb1c.pk001.k23	(SEQ ID NO:12)	(184)	IIDVETTKENSRLOFIVALSISQCDILOACKNIGHKVKGDLIEPED--	300
r10n.pk117.i23	(SEQ ID NO:14)	(111)	AEKLNATAEATGLVSVCMPTNSTSEANVNVKVC-----AER--	
rr1.pk0050.h8	(SEQ ID NO:16)	(158)	AEKLNATAEATGLVSVCMPTNSTSEANVNVKVC-----AER--	
s11.pk0128.h7	(SEQ ID NO:18)	(196)	IASAEIDKONGRFQIVGVISGKYDVCKSVAKKVKDGHILDD--	
wdk5c.pk005.f22	(SEQ ID NO:20)	(138)	ARDAEAPARNVOLDVIVISGRMDVQACRNLAQKVDKLLRPED--	
M.lutUPPS	(SEQ ID NO:24)	(175)	-----ISETHFNEYLF--ANMDEEII	301
Yeastsrt1	(SEQ ID NO:28)	(223)	-----R-----INIRKFTNKMVG-FHSNKCEII	
Yeastrer2	(SEQ ID NO:26)	(189)	-----TLASHLYTAGVPLDII	
dms2c.pk005.c7	(SEQ ID NO:2)	(212)	-----INEFTIENLGNPCIPPHDII	
ecs1c.pk009.p19	(SEQ ID NO:4)	(156)	-----IDEKYFKQGLGKMKIDFVYDII	
ehb2c.pk001.i10	(SEQ ID NO:6)	(188)	---QELEEANATGSSTVIQTENMESYSIGIKLVLDKNIYIN--YEVVI	
ehb2c.pk001.d17	(SEQ ID NO:8)	(188)	---QELEEANATGSSTVIQTENMESYSIGIKLVLDKNIYIN--YEVVI	
ehb2c.pk001.o18	(SEQ ID NO:10)	(192)	EAEQEFKEANGTG-NSVIPQKTESYSGINLADLKNIYVN--PHEDVI	
vdb1c.pk001.k23	(SEQ ID NO:12)	(232)	-----INKSLEIEQLQNCNCTEFEDII	
r10n.pk117.i23	(SEQ ID NO:14)	(150)	-----R---DILQREDADSVANGGVYSDISVADLDRHMYSGCDDIIV	
rr1.pk0050.h8	(SEQ ID NO:16)	(197)	-----R---DILQREDADSVANGGVYSDISVADLDRHMYSGCDDIIV	
s11.pk0128.h7	(SEQ ID NO:18)	(244)	-----INENIIEQLQNCNCTEFEDII	
wdk5c.pk005.f22	(SEQ ID NO:20)	(186)	-----IDESLIFADLQI--SETSCDII	
M.lutUPPS	(SEQ ID NO:24)	(197)	RTSGEIRSNFIMOCYS--EFVIEEFWIDNEESLAQCISIYQNRHR	350
Yeastsrt1	(SEQ ID NO:28)	(247)	RTSGHRPSDYMMOCVHEN-ATIESSTTMEISSFFAMYLMLKWSFFST	
Yeastrer2	(SEQ ID NO:26)	(207)	RTSGVSEISDIIIMOCASSKGVRIELLCTWEEQPIRMAWILLKFSFKHS	
dms2c.pk005.c7	(SEQ ID NO:2)	(236)	RTSGELVSNFIMOCAYT--EYVSETMEDEDELLHGLNTECHRRR	
ecs1c.pk009.p19	(SEQ ID NO:4)	(180)	RTSGEIRSNFIMOCAYS--EYVETPKYFDEGENDLIELLAKQVRK	
ehb2c.pk001.i10	(SEQ ID NO:6)	(233)	RTSGEIRSNFIMOCATTNC--IYSPYAMDEILRHVWMSVINQRHYS	
ehb2c.pk001.d17	(SEQ ID NO:8)	(233)	RTSGEIRSNFIMOCATTNC--IYSPYAMDEILRHVWMSVINQRHYS	
ehb2c.pk001.o18	(SEQ ID NO:10)	(239)	RTSGELSNFIMOCATSN--IYSPFAEMDEILRHVWMSVINQRHYS	
vdb1c.pk001.k23	(SEQ ID NO:12)	(256)	RTSGELVSNFIMOCAYT--EYVSETMEDEDELLHGLNTECHRRR	
r10n.pk117.i23	(SEQ ID NO:14)	(192)	RTSGEIRSNFIMOCATTFS--HQNPPPWDESFKHLWAILOYQRVHP	
rr1.pk0050.h8	(SEQ ID NO:16)	(239)	RTSGEIRSNFIMOCATTFS--HQNPPPWDESFKHLWAILOYQRVHP	
s11.pk0128.h7	(SEQ ID NO:18)	(268)	RTSGEIRSNFIMOCAYT--EYVYANREIMDEGKDEFDAI LSSEQQR	
wdk5c.pk005.f22	(SEQ ID NO:20)	(208)	RTSGEIRSNFIMOCAYS--EYVETTTTIDEGEAQYLOQMMAEQRDR	

18/24

	351	RFGL	398
M.lutUPPS	(SEQ ID NO:24)	(245)	
Yeaststl	(SEQ ID NO:28)	(296)	
Yeastrer2	(SEQ ID NO:26)	(257)	
dms2c.pk005.c7	(SEQ ID NO:2)	(284)	
ecslc.pk009.p19	(SEQ ID NO:4)	(228)	
ehb2c.pk001.i10	(SEQ ID NO:6)	(281)	
ehb2c.pk001.d17	(SEQ ID NO:8)	(281)	
ehb2c.pk001.o18	(SEQ ID NO:10)	(287)	
vdb1c.pk001.k23	(SEQ ID NO:12)	(304)	
r10n.pk117.i23	(SEQ ID NO:14)	(240)	
rr1.pk0050.h8	(SEQ ID NO:16)	(287)	
sl1.pk0128.h7	(SEQ ID NO:18)	(316)	
wdk5c.pk005.f22	(SEQ ID NO:20)	(256)	

FIG. 4-4

19/24

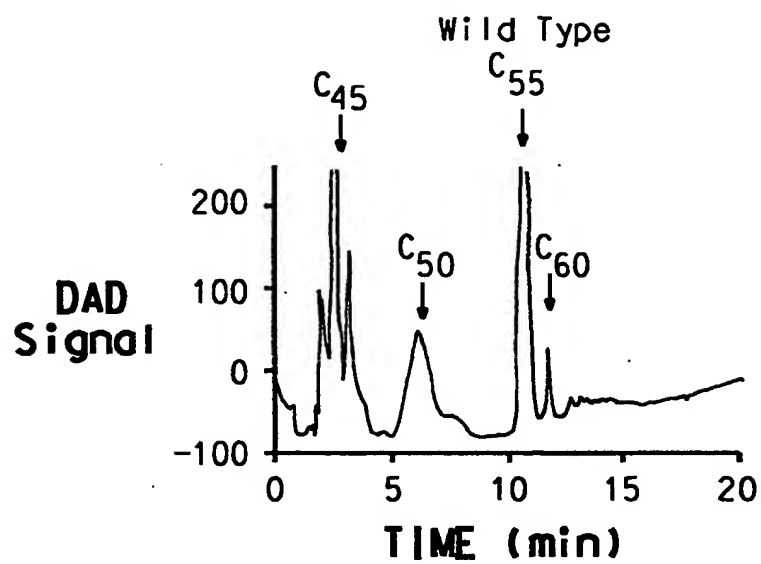


FIG. 5A

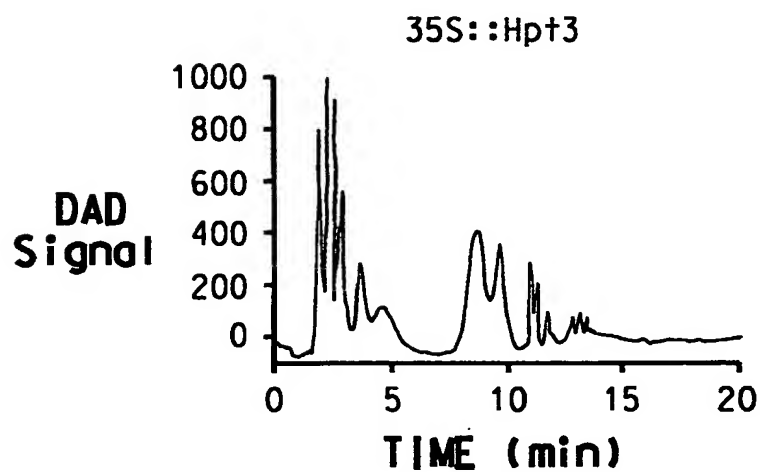


FIG. 5B

20/24

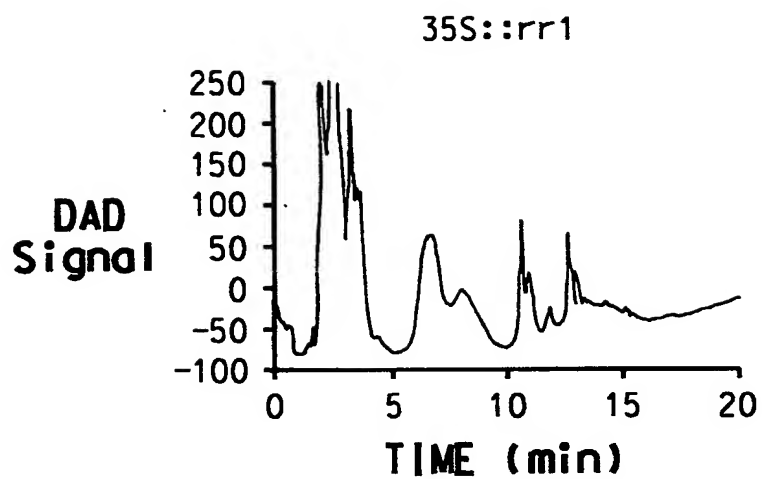


FIG. 5C

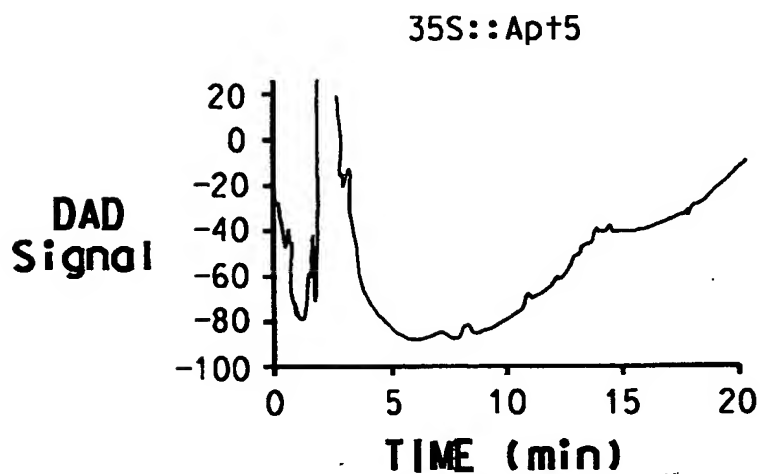


FIG. 5D

21/24

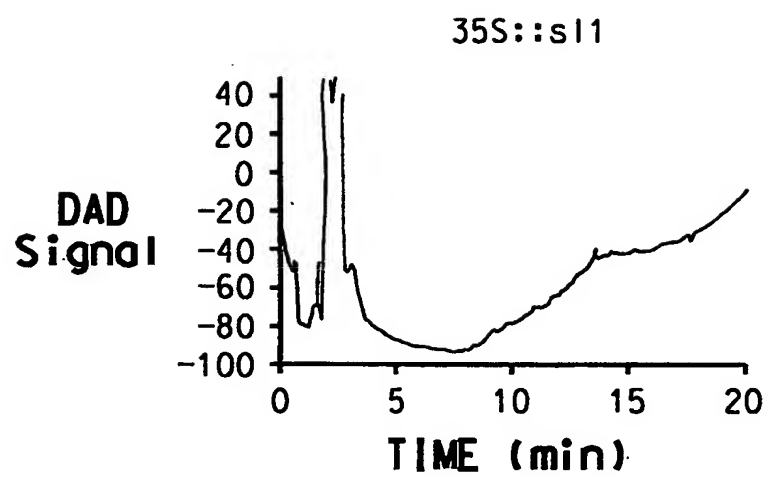


FIG. 5E

22/24

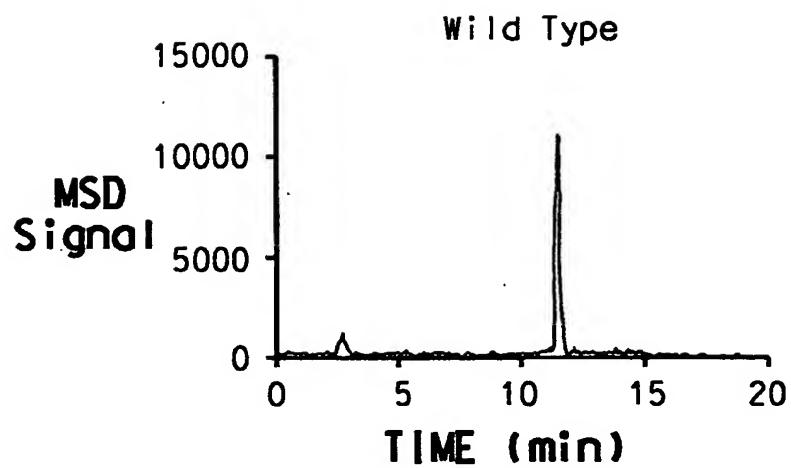


FIG. 6A

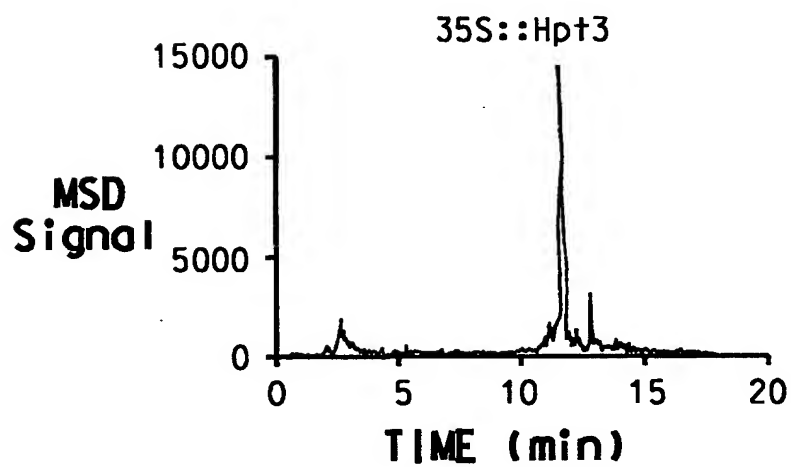


FIG. 6B

23/24

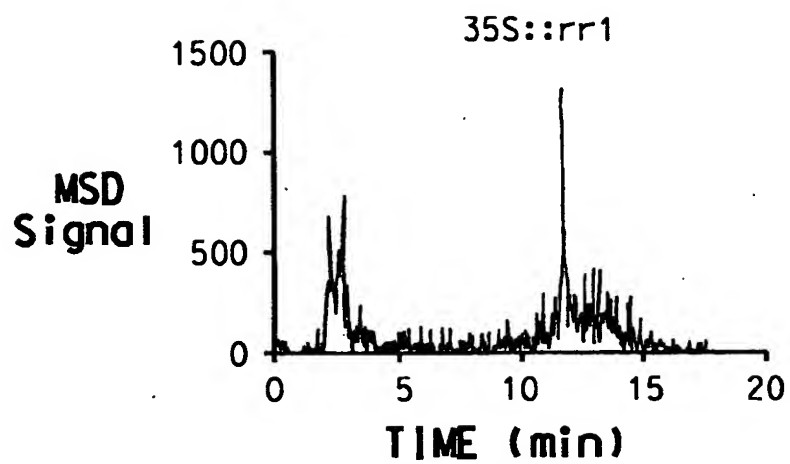


FIG. 6C

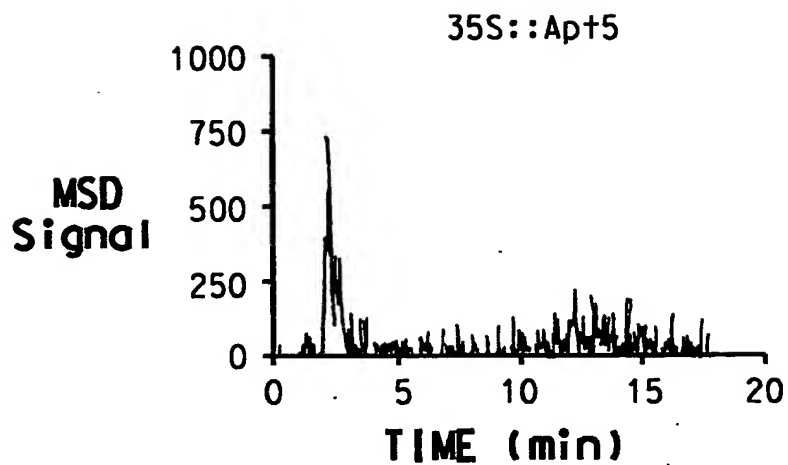


FIG. 6D

24/24

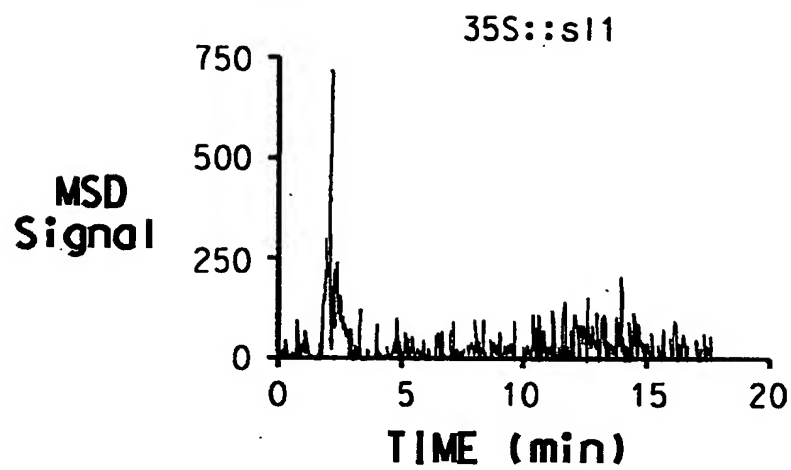


FIG. 6E

SEQUENCE LISTING

<110> E.I. du Pont de Nemours and Company

<120> cis-Prenyltransferases from Plants

<130> BC1019 PCT

<140>

<141>

<150> 60/155,046

<151> 1999-09-21

<160> 37

<170> Microsoft Office 97

<210> 1

<211> 1388

<212> DNA

<213> Dimorphotheca

<400> 1

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gaattgtgag cggataacaa tttcacacag gaaacagcta tgaccatgat tacgccaagc 180
gcgcaattaa ccctcactaa agggaacaaa aggctggagc tccaccgcgg tggcgggccgc 240
tctagaacta gtggatcccc cgggctgcag gaattcggca cgagcttaaa taatgcttaa 300
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ccaccgtggt ctttatgtat tcaaccaatc agacaccact ggaggtggaa ttaattcgct 420
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gatcatggat ggaaacagga gatgggctcg atcacgtggg ttaatgccgg atgctgggta 540
catggaaggt gcacgctcat tgaaggtgat ggtggaattg tgcgtaaaat ggggaattca 600
agtccttact gtgtttgcct tctcagctga taactgggta agacccaaag ttgaagttga 660
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cattacatat gctgaaaaca tcacgaagaa caactcacia ctcaatcttg ttgtagcaat 840
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<210> 2

<211> 287

<212> PRT

<213> Dimorphotheca

<400> 2

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Met Leu Asn Leu Pro Leu Tyr Leu Pro Lys Tyr Pro Cys Tyr Phe Pro
 1                      5                      10                      15

Ala Ser Leu Ser Thr Asn His His Arg Gly Leu Tyr Val Phe Asn Gln
                20                      25                      30

Ser Asp Thr Thr Gly Gly Gly Ile Asn Ser Leu Glu Glu Arg Ile Thr
 35                      40                      45

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Pro Ala Gly Leu Lys His Glu Leu Met Pro Lys His Val Ala Val Ile
 50 55 60
 Met Asp Gly Asn Arg Arg Trp Ala Arg Ser Arg Gly Leu Met Pro Asp
 65 70 75 80
 Ala Gly Tyr Met Glu Gly Ala Arg Ser Leu Lys Val Met Val Glu Leu
 85 90 95
 Cys Arg Lys Trp Gly Ile Gln Val Leu Thr Val Phe Ala Phe Ser Ala
 100 105 110
 Asp Asn Trp Leu Arg Pro Lys Val Glu Val Asp Phe Leu Met Gly Leu
 115 120 125
 Ile Glu Ser Val Leu Lys Asp Glu Val Val His Met Ile Lys Glu Gly
 130 135 140
 Ile Gln Leu Ser Val Ile Gly Asp Thr Ser Lys Leu Pro Lys Ser Val
 145 150 155 160
 Lys Arg Ile Ile Thr Tyr Ala Glu Asn Ile Thr Lys Asn Asn Ser Gln
 165 170 175
 Leu Asn Leu Val Val Ala Ile Asn Tyr Ser Gly Lys Tyr Asp Ile Val
 180 185 190
 Gln Ala Cys Gln Ser Ile Ala Leu Lys Val Lys Asp Gly Val Ile Gln
 195 200 205
 Pro Glu Glu Ile Asn Glu Phe Thr Ile Glu Asn Glu Leu Gly Thr Asn
 210 215 220
 Cys Ile Pro Phe Pro His Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu
 225 230 235 240
 Leu Arg Val Ser Asn Phe Phe Leu Trp Gln Leu Ala Tyr Thr Glu Leu
 245 250 255
 Tyr Phe Ser Glu Thr Leu Trp Pro Asp Phe Gly Glu Asp Glu Leu Leu
 260 265 270
 His Ala Leu Asn Thr Phe Gln His Arg Arg Arg Arg Tyr Gly Gly
 275 280 285

<210> 3

<211> 1082

<212> DNA

<213> Calendula officinalis

<400> 3

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 ttacaaatat atcaacggtt ttgagcaatg aaaataccaa actgaaaacc aaaaaaagaa 180
 gaagtagaat taccaggggg tctcgaagaa gaactaatgc caaaacacgt tgcattcata 240
 atggatggaa accgtcgatg ggcgggtggaa aaaggttggt ctccaatgac ggggtcatagt 300
 gccatgagaa agacgcttca atctctcctt tttcgatggt ccaaattcaa aatcaaagcg 360
 gtatcgattt atgcattttc taccgaaaat tggactcgcc cgaaggaaga agttgatttc 420
 ctaatggaga tgtatgaaga tttattgagg acagatgctg aggagctctt aagtcttggt 480
 tgtcgagtaa gcataatggg gaaaaagacc aaccttccga aatcactaca aaagttatgc 540
 atcgaaatag aagaaaaatc aagagccaat tcaggaaccc atgttaacta tgcactcaac 600
 tacagtggaa aatacgacat aatcgaagct tgtaaaagcg tcgctacaaa agtcaaggat 660


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ggtgttatta ttccaaaaca gatcgacgaa aaatatttca aacaagaact cggtagcaaaa 720
atgatcgatt ttccttaccc tgacctagtt atacgtacaa gcggggaaat taggcttagt 780
aatttcacgc tatggcagat ggcgtatagc gagctttatt tcacggataa atactttccg 840
gattttgggg aaaatgatct tatcgaggct ttacttgcac ttcaaaaagt gcgtaaatgt 900
taataacttg ttgtgggtaa gacgagtgtg gtagaatatc aataaatgac tcgtttcggc 960
ggcgttgtgt atgccacatt atatgtctta gtgtctatca gaattcgaat ttgatttata 1020
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<210> 4

<211> 228

<212> PRT

<213> Calendula officinalis

<400> 4

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Met Pro Lys His Val Ala Phe Ile Met Asp Gly Asn Arg Arg Trp Ala
 1             5             10             15
Val Glu Lys Gly Trp Ser Pro Met Thr Gly His Ser Ala Met Arg Lys
          20             25             30
Thr Leu Gln Ser Leu Leu Phe Arg Cys Ser Lys Phe Lys Ile Lys Ala
          35             40             45
Val Ser Ile Tyr Ala Phe Ser Thr Glu Asn Trp Thr Arg Pro Lys Glu
          50             55             60
Glu Val Asp Phe Leu Met Glu Met Tyr Glu Asp Leu Leu Arg Thr Asp
 65             70             75             80
Ala Glu Glu Leu Leu Ser Leu Gly Cys Arg Val Ser Ile Met Gly Lys
          85             90             95
Lys Thr Asn Leu Pro Lys Ser Leu Gln Lys Leu Cys Ile Glu Ile Glu
          100            105            110
Glu Lys Ser Arg Ala Asn Ser Gly Thr His Val Asn Tyr Ala Leu Asn
          115            120            125
Tyr Ser Gly Lys Tyr Asp Ile Ile Glu Ala Cys Lys Ser Val Ala Thr
          130            135            140
Lys Val Lys Asp Gly Val Ile Ile Pro Lys Gln Ile Asp Glu Lys Tyr
          145            150            155            160
Phe Lys Gln Glu Leu Gly Thr Lys Met Ile Asp Phe Pro Tyr Pro Asp
          165            170            175
Leu Val Ile Arg Thr Ser Gly Glu Ile Arg Leu Ser Asn Phe Met Leu
          180            185            190
Trp Gln Met Ala Tyr Ser Glu Leu Tyr Phe Thr Asp Lys Tyr Phe Pro
          195            200            205
Asp Phe Gly Glu Asn Asp Leu Ile Glu Ala Leu Leu Ala Phe Gln Lys
          210            215            220
Val Arg Lys Cys
225

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<210> 5

<211> 1071

<212> DNA

<213> Hevea brasiliensis

<400> 5

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taagtcagtg atttaaggaa aatggaatta tacaacgggt agaggccaag tgtgttcaga 180
cttttaggga agtatatgag aaaaggggta tatagcatcc taaccagggt tcccatccct 240
actcatattg ccttcatatt ggatggaaac aggaggtttg ctaagaagca taaactgcca 300
gaaggagggt gtcataaggc tggattttta gctccttctga acgtactaac ttattgctat 360
gagttaggag tgaaatatgc gactatctat gccttttagca tcgataattt tcgaaggaaa 420
cctcatgagg ttcagtacgt aatggatcta atgctggaga agattgaagg gatgatcatg 480
gaagaaagta tcatcaatgc atatgatatt tgcgtacgtt ttgtgggtaa cctgaagcct 540
ttaagtgagc ccgtcaagac cgcagcagat aagattatga gggctactgc caacaattcc 600
aaatgtgtgc ttctcattgc tgtatgctat acttcaactg atgagatcgt gcatgctgtt 660
gaagaatcct ctgaattgaa ctccaatgaa gtttgtaaca atcaagaatt ggaggaggca 720
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aaacttgtag accttgagaa aaacacctac ataaatcctt atcctgatgt tctgattcga 840
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tattctcctt atgcactgtg gccagagatt ggtcttcgac acgtggtgtg gtcagtaatt 960
aacttccaac gtcattattc ttacttgagg aaacataagg aataactaaa ataatttggt 1020
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<210> 6

<211> 290

<212> PRT

<213> Hevea brasiliensis

<400> 6

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Met Glu Leu Tyr Asn Gly Glu Arg Pro Ser Val Phe Arg Leu Leu Gly
 1             5             10             15

Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile
      20             25             30

Pro Thr His Ile Ala Phe Ile Leu Asp Gly Asn Arg Arg Phe Ala Lys
      35             40             45

Lys His Lys Leu Pro Glu Gly Gly Gly His Lys Ala Gly Phe Leu Ala
      50             55             60

Leu Leu Asn Val Leu Thr Tyr Cys Tyr Glu Leu Gly Val Lys Tyr Ala
      65             70             75             80

Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu
      85             90             95

Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile
      100            105            110

Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val
      115            120            125

Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys
      130            135            140

Ile Met Arg Ala Thr Ala Asn Asn Ser Lys Cys Val Leu Leu Ile Ala
      145            150            155            160

Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser
      165            170            175

Ser Glu Leu Asn Ser Asn Glu Val Cys Asn Asn Gln Glu Leu Glu Glu
      180            185            190

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Ala Asn Ala Thr Gly Ser Ser Thr Val Ile Gln Thr Glu Asn Met Glu
 195 200 205

Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile
 210 215 220

Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu
 225 230 235 240

Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro
 245 250 255

Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val
 260 265 270

Ile Asn Phe Gln Arg His Tyr Ser Tyr Leu Glu Lys His Lys Glu Tyr
 275 280 285

Leu Lys
 290

<210> 7
 <211> 1000
 <212> DNA
 <213> Hevea brasiliensis

<400> 7
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 tccctactca tattgccttc atattggatg gaaacaggag gtttgctaag aagcataaac 180
 tgccagaagg aggtggtcat aaggctggat ttttagctct tctgaacgta ctaacttatt 240
 gctatgagtt aggagtgaat tatgcgacta tctatgcctt tagcatcgat aattttcgaa 300
 ggaaacctca tgaggttcag tacgtaatgg atctaattgct ggagaagatt gaagggatga 360
 tcatggaaga aagtatcatc aatgcatatg atatttgctg acgttttgtg ggtaacctga 420
 agctttttaag tgagccagtc aagaccgcag cagataagat tatgagggct actgccaaca 480
 attccaaatg tgtgcttctc attgctgtat gctatacttc aactgatgag atcgtgcatg 540
 ctgttgaaga atcctctgaa ttgaactcca atgaagtgtg taacaatcaa gaattggagg 600
 aggcaaatgc aactggaagc agtactgtga ttcaaactga gaacatggag tcgtattctg 660
 gaataaaaact tgtagacctt gagaaaaaca cctacataaa tccttatcct gatgttctga 720
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<210> 8
 <211> 290
 <212> PRT
 <213> Hevea brasiliensis

<400> 8
 Met Glu Leu Tyr Asn Gly Glu Arg Pro Ser Val Phe Arg Leu Leu Glu.
 1 5 10 15

Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile
 20 25 30

Pro Thr His Ile Ala Phe Ile Leu Asp Gly Asn Arg Arg Phe Ala Lys
 35 40 45

Lys His Lys Leu Pro Glu Gly Gly Gly His Lys Ala Gly Phe Leu Ala
 50 55 60

Leu Leu Asn Val Leu Thr Tyr Cys Tyr Glu Leu Gly Val Lys Tyr Ala
 65 70 75 80
 Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu
 85 90 95
 Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile
 100 105 110
 Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val
 115 120 125
 Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys
 130 135 140
 Ile Met Arg Ala Thr Ala Asn Asn Ser Lys Cys Val Leu Leu Ile Ala
 145 150 155 160
 Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser
 165 170 175
 Ser Glu Leu Asn Ser Asn Glu Val Cys Asn Asn Gln Glu Leu Glu Glu
 180 185 190
 Ala Asn Ala Thr Gly Ser Ser Thr Val Ile Gln Thr Glu Asn Met Glu
 195 200 205
 Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile
 210 215 220
 Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu
 225 230 235 240
 Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro
 245 250 255
 Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val
 260 265 270
 Ile Asn Phe Gln Arg His Tyr Ser Tyr Leu Glu Lys His Lys Glu Tyr
 275 280 285
 Leu Lys
 290

<210> 9

<211> 1000

<212> DNA

<213> Hevea brasiliensis

<400> 9

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 catgagaaaa ggggttatata gcatcctaac ccaagggtccc atccctactc atcttgctt 180
 cataatggat ggaaaccgga ggtttgctaa gaagcacaaa atgaaagaag cagaagggtta 240
 taaggcagga tatttagctc ttctgagaac actaacttat tgctatgagt tgggagtgag 300
 gtatgtaacc atttatgcct ttagcattga taattttcga aggcaacctc gtgaggttca 360
 gtgcgtaatg aatctaata tggagaagat tgaagagatt atcgtggaag aaagtatcat 420
 gaatgcatat gatgttggcg tacgtattgt gggtaacctg aatcttttag atgagccaat 480
 caggatcgca gcagaaaaga ttatgagggc tactgccaat aattccgggt ttgtgcttct 540
 cattgctgta gcctatagtt caactgatga gatcgggcat gctgttgaag aatcctctaa 600
 agacaaattg aactccaatg aagtttgcaa caatgggatt gaagctgaac aggaatttaa 660
 ggaggcaaac ggaaccggaa acagtgtgat tccagttcag aagacggagt catattctgg 720
 aataaatctt gcagaccttg agaaaaacac ctacgtaaat cctcatcctg atgtcttgat 780

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tcgaacttct gggttgagcc gtctaagtaa ctacctactt tggcagacta gtaattgcat 840
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aatgaacttc caacgtcatc attcttattt ggagaagcat aaggaatatt taaaataatt 960
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<210> 10

<211> 296

<212> PRT

<213> Hevea brasiliensis

<400> 10

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Met Glu Ile Tyr Thr Gly Gln Arg Pro Ser Val Phe Arg Ile Phe Gly
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Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile
          20           25           30
Pro Thr His Leu Ala Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Lys
          35           40           45
Lys His Lys Met Lys Glu Ala Glu Gly Tyr Lys Ala Gly Tyr Leu Ala
          50           55           60
Leu Leu Arg Thr Leu Thr Tyr Cys Tyr Glu Leu Gly Val Arg Tyr Val
 65           70           75           80
Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Gln Pro Arg Glu
          85           90           95
Val Gln Cys Val Met Asn Leu Met Met Glu Lys Ile Glu Glu Ile Ile
          100          105          110
Val Glu Glu Ser Ile Met Asn Ala Tyr Asp Val Gly Val Arg Ile Val
          115          120          125
Gly Asn Leu Asn Leu Leu Asp Glu Pro Ile Arg Ile Ala Ala Glu Lys
          130          135          140
Ile Met Arg Ala Thr Ala Asn Asn Ser Gly Phe Val Leu Leu Ile Ala
          145          150          155          160
Val Ala Tyr Ser Ser Thr Asp Glu Ile Gly His Ala Val Glu Glu Ser
          165          170          175
Ser Lys Asp Lys Leu Asn Ser Asn Glu Val Cys Asn Asn Gly Ile Glu
          180          185          190
Ala Glu Gln Glu Phe Lys Glu Ala Asn Gly Thr Gly Asn Ser Val Ile
          195          200          205
Pro Val Gln Lys Thr Glu Ser Tyr Ser Gly Ile Asn Leu Ala Asp Leu
          210          215          220
Glu Lys Asn Thr Tyr Val Asn Pro His Pro Asp Val Leu Ile Arg Thr
          225          230          235          240
Ser Gly Leu Ser Arg Leu Ser Asn Tyr Leu Leu Trp Gln Thr Ser Asn
          245          250          255
Cys Ile Leu Tyr Ser Pro Phe Ala Leu Trp Pro Glu Ile Gly Leu Arg
          260          265          270
His Leu Val Trp Thr Val Met Asn Phe Gln Arg His His Ser Tyr Leu
          275          280          285

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Glu Lys His Lys Glu Tyr Leu Lys
290 295

<210> 11
<211> 1232
<212> DNA
<213> Vitis sp

<400> 11
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aagtaacaga atcgattcat ttctttttcc tccaatctca gttcccagat ttcacaaact 180
tcgcacagct aaaactgatg tagttgggga agaagaagca agagaagtaa acgagagagc 240
ggaggaattt cgggacgggc ttccggagaga actgatgccg gaacacgtgg ccgtcattat 300
ggacgggaac gtgaggtggg cacagaagag ggggttgccg gcggcgctcg gtcaccaagc 360
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ctcgggttttc gcatttttct atgataattg gtctcgttcc gaaggggagg ttggttttct 480
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cgagtgtcgt gattggggat ttgtcaaagc ttctgagcaa ctgcaactga taattgatgt 600
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gcgaaactga gtttactaat tacatataga tccccaactt ctgctccatt catatggaga 1020
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caacctatac tccattcata tggaaaactt gtaccattat atgaaactca ttcttcagaa 1140
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atacttttac ttcaaaaaaa aaaaaaaa aa 1232

<210> 12
<211> 309
<212> PRT
<213> Vitis sp

<400> 12
Met Leu Ser Phe Arg Phe Pro Ile Ser Ala Asp Asn Ala Arg His Thr
1 5 10 15
Phe Lys Ser Lys His Ser Ser Cys Thr Phe Arg Ser Asn Arg Ile Asp
20 25 30
Ser Phe Ser Phe Pro Pro Ile Ser Val Pro Arg Phe His Lys Leu Arg
35 40 45
Thr Ala Lys Thr Asp Val Val Gly Glu Glu Glu Ala Arg Glu Val Asn
50 55 60
Glu Arg Ala Glu Glu Phe Pro Asp Gly Leu Arg Arg Glu Leu Met Pro
65 70 75 80
Glu His Val Ala Val Ile Met Asp Gly Asn Val Arg Trp Ala Gln Lys
85 90 95
Arg Gly Leu Pro Ala Ala Ser Gly His Gln Ala Gly Val Arg Ser Leu
100 105 110
Arg Glu Leu Val Glu Leu Cys Cys Lys Trp Gly Ile Lys Val Leu Ser
115 120 125

Val Phe Ala Phe Ser Tyr Asp Asn Trp Ser Arg Ser Glu Gly Glu Val
 130 135 140

Gly Phe Leu Met Ser Leu Ile Glu Arg Val Val Lys Ala Glu Leu Pro
 145 150 155 160

Ile Leu Gly Gly Lys Ala Phe Glu Cys Arg Asp Trp Gly Phe Val Lys
 165 170 175

Ala Ser Glu Gln Leu Gln Leu Ile Ile Asp Val Glu Glu Thr Thr Lys
 180 185 190

Glu Asn Ser Arg Leu Gln Phe Ile Val Ala Leu Ser Tyr Ser Gly Gln
 195 200 205

Cys Asp Ile Leu Gln Ala Cys Lys Asn Ile Gly His Lys Val Lys Asp
 210 215 220

Gly Leu Ile Glu Pro Glu Asp Ile Asn Lys Ser Leu Ile Glu Gln Glu
 225 230 235 240

Leu Gln Thr Asn Cys Thr Glu Phe Pro Phe Pro Asp Leu Leu Ile Arg
 245 250 255

Thr Ser Gly Glu Leu Arg Val Ser Asn Phe Met Leu Trp Gln Ile Ala
 260 265 270

Tyr Thr Glu Leu Cys Phe Phe Ser Thr Leu Trp Pro Asp Phe Gly Lys
 275 280 285

Asp Glu Phe Val Glu Ala Leu Ser Ser Phe Gln Lys Arg Gln Arg Arg
 290 295 300

Tyr Gly Gly Arg Asn
 305

<210> 13
 <211> 1021
 <212> DNA
 <213> Oryza sativa

<400> 13
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 catattgcat ttattatgga tggtaaccgt agatatgcta aattcaggag tatccaggaa 120
 ggctctgggc acaggggtggg cttctctgct ctcattgcca gcctgctcta ctgctatgaa 180
 atgggcgtga agtatatcac ggtgtatgca tttagcatcg ataattttaa gcgagatccg 240
 actgaggtga aatccttgat ggagttaatg gaggaaaaaga tcaatgaaact gctagaaaac 300
 agaaatgtca tcaacaaggt taactgtaag atcaacttct gggggaactt ggacatgttg 360
 agcaaatcag tgagggtagc agctgagaaa ctgatggcta ccactgctga aaacacggga 420
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 aatggtgtgt attcagacat ttcagtggca gatctggacc gccatatgta cagcgtggt 600
 tgccccgata ctgacattgt gatccggacc tcaggtgaga ctgcctgag caatttcctt 660
 ctgtggcaga cgacgttcag tcatttgtag aatccagacc ctctttggcc ggagttctct 720
 ttcaagcacc ttgtctgggc catactccag taccaaagag ttcacccttc tattgagcaa 780
 agcagaaatc tggctaagaa gcagctgtaa tcacatcctc cctgggagga gatagaaacc 840
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 tatgaaatat ataaaggata gctatgccat tgtatgcttg aacatgtgta tgcttgagtt 960
 ggtccaaatg tgtgaaatgt aataacattt ggtctaaaaa aaaaaaaaaa aaaaaaaaaa 1020
 a 1021

<210> 14
 <211> 252
 <212> PRT
 <213> Oryza sativa

<400> 14
 Met Pro Lys His Ile Ala Phe Ile Met Asp Gly Asn Arg Arg Tyr Ala
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 Lys Phe Arg Ser Ile Gln Glu Gly Ser Gly His Arg Val Gly Phe Ser
 20 25 30
 Ala Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr
 35 40 45
 Ile Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr
 50 55 60
 Glu Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu
 65 70 75 80
 Leu Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe
 85 90 95
 Trp Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu
 100 105 110
 Lys Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val
 115 120 125
 Cys Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys
 130 135 140
 Val Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser
 145 150 155 160
 Val Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp
 165 170 175
 Arg His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg
 180 185 190
 Thr Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr
 195 200 205
 Phe Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe
 210 215 220
 Lys His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser
 225 230 235 240
 Ile Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu
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 <211> 900
 <212> DNA
 <213> Oryza sativa

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 gctgtcctct cgtatggccc aatgcctaag catattgcat ttattatgga tggtaaccgt 180


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cagagggagg atgctgacag tgttgcaat aatggtgtgt attcagacat ttcagtggca 660
gatctggacc gccatatgta cagcgctggg tgccccgac ctgacattgt gatccggacc 720
tcaggtgaga ctcgcctgag caatttcctt ctgtggcaga cgacgttcag tcatttgtag 780
aatccagacc ctctttggcc ggagttctct ttcaagcacc ttgtctgggc catactccag 840
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<210> 16

<211> 299

<212> PRT

<213> *Oryza sativa*

<400> 16

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Met Leu Gly Ser Leu Met Ser Tyr Leu Pro Ser Val Asp Ser Lys Thr
  1                      5                      10                      15

Glu Asn Thr Asp Glu Leu Ile Ala Thr Gly Val Leu Ala Ser Leu Gln
      20                      25                      30

Asn Phe Ile Arg Lys Cys Ile Val Ala Val Leu Ser Tyr Gly Pro Met
      35                      40                      45

Pro Lys His Ile Ala Phe Ile Met Asp Gly Asn Arg Arg Tyr Ala Lys
      50                      55                      60

Phe Arg Ser Ile Gln Glu Gly Ser Gly His Arg Val Gly Phe Ser Ala
      65                      70                      75                      80

Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr Ile
      85                      90                      95

Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr Glu
      100                      105                      110

Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu Leu
      115                      120                      125

Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe Trp
      130                      135                      140

Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu Lys
      145                      150                      155                      160

Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val Cys
      165                      170                      175

Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys Val
      180                      185                      190

Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser Val
      195                      200                      205

Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp Arg
      210                      215                      220

His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg Thr
      225                      230                      235                      240

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Ser	Gly	Glu	Thr	Arg 245	Leu	Ser	Asn	Phe	Leu 250	Leu	Trp	Gln	Thr	Thr 255	Phe
Ser	His	Leu	Gln 260	Asn	Pro	Asp	Pro	Leu 265	Trp	Pro	Glu	Phe	Ser 270	Phe	Lys
His	Leu	Val 275	Trp	Ala	Ile	Leu	Gln 280	Tyr	Gln	Arg	Val	His 285	Pro	Ser	Ile
Glu	Gln 290	Ser	Arg	Asn	Leu 295	Ala	Lys	Lys	Gln	Leu					

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<210> 17
<211> 1028
<212> DNA
<213> Glycine max
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cccaaacaca	gagtccttate	gtctcgaagc	gcggttcgcg	cattgcgaag	tgtcacgctg		240
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ggaggtgggc	gaaggtgaag	gggctgccac	catcggcggg	gcaccaggcg	ggggtgcaat		420
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tgattggaga	ttcatacaag	tgcctgagt	ctttaaaaag	aatgatagct	agtgcagaag		660
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atgatgttgt	gcaagcatgt	aaaagtgtag	ccaagaaagt	caaagatggt	cacattcact		780
tggtgacat	aaacgaaaac	attattgaac	aagaattgga	aactaattgt	actgagtttc		840
cttatcctga	tctactaata	cgaactagtg	gcgagcttag	agtgaagtaac	ttcttggtgt		900
ggcaattagc	ctacacagaa	ctttatttta	atcggaact	ctggccagat	tttggaagg		960
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attcataa							1028

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<210> 18
<211> 322
<212> PRT
<213> Glycine max
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Met Phe Ser Leu Arg Leu Pro Ile Pro Leu Val Lys Thr Pro Pro Ser
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Pro Ser Cys Tyr Tyr Ser His Tyr Tyr His Tyr Arg Tyr Arg Tyr Arg
          20          25          30
Cys Tyr His Pro Phe His His Arg Ser Gln Thr Gln Ser Leu Ile Val
          35          40          45
Ser Lys Arg Gly Ser Ala Ile Ala Lys Cys His Ala Asp Ser Val Thr
          50          55          60
Leu Arg Asp Asp Gly Val Ser Leu Ala Gln Glu Ser Leu Glu Pro Leu
          65          70          75          80
Pro Ala Glu Leu Ala Ala Glu Met Met Pro Lys His Val Ala Val Ile
          85          90          95

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Met Asp Gly Asn Gly Arg Trp Ala Lys Val Lys Gly Leu Pro Pro Ser
100 105 110

Ala Gly His Gln Ala Gly Val Gln Ser Leu Arg Lys Met Val Arg Leu
115 120 125

Cys Cys Ser Trp Gly Ile Lys Val Leu Thr Val Phe Ala Phe Ser Thr
130 135 140

Asp Asn Trp Val Arg Pro Lys Val Glu Val Asp Phe Leu Met Arg Leu
145 150 155 160

Phe Glu Arg Thr Ile Asn Ser Glu Val Gln Thr Phe Lys Arg Glu Gly
165 170 175

Ile Arg Ile Ser Val Ile Gly Asp Ser Ser Arg Leu Pro Glu Ser Leu
180 185 190

Lys Arg Met Ile Ala Ser Ala Glu Glu Asp Thr Lys Gln Asn Ser Arg
195 200 205

Phe Gln Leu Ile Val Ala Val Gly Tyr Ser Gly Lys Tyr Asp Val Val
210 215 220

Gln Ala Cys Lys Ser Val Ala Lys Lys Val Lys Asp Gly His Ile His
225 230 235 240

Leu Asp Asp Ile Asn Glu Asn Ile Ile Glu Gln Glu Leu Glu Thr Asn
245 250 255

Cys Thr Glu Phe Pro Tyr Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu
260 265 270

Leu Arg Val Ser Asn Phe Leu Leu Trp Gln Leu Ala Tyr Thr Glu Leu
275 280 285

Tyr Phe Asn Arg Glu Leu Trp Pro Asp Phe Gly Lys Asp Glu Phe Val
290 295 300

Asp Ala Leu Ser Ser Phe Gln Gln Arg Gln Arg Arg Tyr Gly Gly Arg
305 310 315 320

His Ser

<210> 19

<211> 1026

<212> DNA

<213> Triticum aestivum

<400> 19

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gccttcgggt	tctcgctcga	gaactggaat	cgcccccaag	cggaggttga	cttcttgatg	300
gccttgatcg	agaggtttat	caacgacaac	ctcgccgagt	tcttgaggga	agggaccctg	360
ctacgtataa	tccgtgaccg	ctcaaggctg	ccgatctctg	tcgagaagac	tcgacgagac	420
gccgaggagg	caacaagaaa	caactcgcat	ctcgatctag	tcctagccat	cagctacagc	480
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gccaatatc	tccaagccat	gatggccttc	cagagcagag	acaggcgctt	tggaagaaga	780
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 ctcaagatgc gtgggtgtact ataggagagg ctactaaaac ttctctccag tgatttttact 960
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<210> 20

<211> 266

<212> PRT

<213> Triticum aestivum

<400> 20

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 20 25 30
 Arg His Val Ala Leu Val Met Asp Gly Asn Ser Arg Trp Ala Ala Ala
 35 40 45
 Arg Gly Leu Pro Pro Thr Asp Gly His Glu His Gly Met Arg Ala Leu
 50 55 60
 Met Arg Thr Val Arg Leu Ser Arg Ala Trp Gly Ile Arg Val Leu Thr
 65 70 75 80
 Ala Phe Gly Phe Ser Leu Glu Asn Trp Asn Arg Pro Lys Ala Glu Val
 85 90 95
 Asp Phe Leu Met Ala Leu Ile Glu Arg Phe Ile Asn Asp Asn Leu Ala
 100 105 110
 Glu Phe Leu Arg Glu Gly Thr Arg Leu Arg Ile Ile Gly Asp Arg Ser
 115 120 125
 Arg Leu Pro Ile Ser Val Gln Lys Thr Ala Arg Asp Ala Glu Glu Ala
 130 135 140
 Thr Arg Asn Asn Ser Gln Leu Asp Leu Val Leu Ala Ile Ser Tyr Ser
 145 150 155 160
 Gly Arg Met Asp Ile Val Gln Ala Cys Arg Asn Leu Ala Gln Lys Val
 165 170 175
 Asp Ala Lys Leu Leu Arg Pro Glu Asp Ile Asp Glu Ser Leu Phe Ala
 180 185 190
 Asp Glu Leu Gln Thr Ser Glu Thr Ser Cys Pro Asp Leu Leu Ile Arg
 195 200 205
 Thr Ser Gly Glu Leu Arg Leu Ser Asn Phe Leu Leu Trp Gln Ser Ala
 210 215 220
 Tyr Ser Glu Leu Phe Phe Thr Asp Thr Leu Trp Pro Asp Phe Gly Glu
 225 230 235 240
 Ala Gln Tyr Leu Gln Ala Met Met Ala Phe Gln Ser Arg Asp Arg Arg
 245 250 255
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<210> 21

<211> 11

<212> PRT
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<220>
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<223> X = any amino acid

<220>
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<223> X = any amino acid

<220>
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<222> (10)
<223> X = any amino acid

<300>
<301> Apfel, C. M.
<302> Use of Genomincs to Indentify Bacterial Undecaprenyl Pyrophosphate Synthetase: Clooning, Expression, and Characterization of the Essential uppS Gene
<303> J. Bacteriol.
<304> 81
<306> 483-492
<307> 1999

<400> 21
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1 5 10

<210> 22
<211> 24
<212> PRT
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<220>
<223> Description of Artificial Sequence: Domain V of published alignment

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<222> (3)
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<222> (7)
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 Leu Trp Gln Xaa Xaa Tyr Xaa Glu
 20

<210> 23
 <211> 750
 <212> DNA
 <213> Micrococcus luteus

<300>
 <301> Shimizu, N.
 <302> Molecular Cloning, Expression, and Purification of Undecprenyl
 Diphosphate Synthase: No Sequence Similarity between E- and
 Z-prenyl Diphosphate Synthases
 <303> J. Biol. Chem.
 <304> 273
 <306> 19476-19481
 <307> 1998

<400> 23
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<210> 24
 <211> 249
 <212> PRT
 <213> Micrococcus luteus

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 20 25 30
 Arg Trp Ala Lys Gln Lys Lys Met Pro Arg Ile Lys Gly His Tyr Glu
 35 40 45
 Gly Met Gln Thr Val Lys Lys Ile Thr Arg Tyr Ala Ser Asp Leu Gly
 50 55 60
 Val Lys Tyr Leu Thr Leu Tyr Ala Phe Ser Thr Glu Asn Trp Ser Arg
 65 70 75 80

Pro Lys Asp Glu Val Asn Tyr Leu Met Lys Leu Pro Gly Asp Phe Leu
85 90 95

Asn Thr Phe Leu Pro Glu Leu Ile Glu Lys Asn Val Lys Val Glu Thr
100 105 110

Ile Gly Phe Ile Asp Asp Leu Pro Asp His Thr Lys Lys Ala Val Leu
115 120 125

Glu Ala Lys Glu Lys Thr Lys His Asn Thr Gly Leu Thr Leu Val Phe
130 135 140

Ala Leu Asn Tyr Gly Gly Arg Lys Glu Ile Ile Ser Ala Val Gln Leu
145 150 155 160

Ile Ala Glu Arg Tyr Lys Ser Gly Glu Ile Ser Leu Asp Glu Ile Ser
165 170 175

Glu Thr His Phe Asn Glu Tyr Leu Phe Thr Ala Asn Met Pro Asp Pro
180 185 190

Glu Leu Leu Ile Arg Thr Ser Gly Glu Glu Arg Leu Ser Asn Phe Leu
195 200 205

Ile Trp Gln Cys Ser Tyr Ser Glu Phe Val Phe Ile Asp Glu Phe Trp
210 215 220

Pro Asp Phe Asn Glu Glu Ser Leu Ala Gln Cys Ile Ser Ile Tyr Gln
225 230 235 240

Asn Arg His Arg Arg Phe Gly Gly Leu
245

<210> 25
<211> 861
<212> DNA
<213> *Saccharomyces cerevisiae*

<300>
<308> AB013497

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<210> 26
<211> 286
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 26

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           20           25           30
Arg His Val Gly Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Arg Lys
           35           40           45
Lys Glu Met Asp Val Lys Glu Gly His Glu Ala Gly Phe Val Ser Met
           50           55           60
Ser Arg Ile Leu Glu Leu Cys Tyr Glu Ala Gly Val Asp Thr Ala Thr
           65           70           75           80
Val Phe Ala Phe Ser Ile Glu Asn Phe Lys Arg Ser Ser Arg Glu Val
           85           90           95
Glu Ser Leu Met Thr Leu Ala Arg Glu Arg Ile Arg Gln Ile Thr Glu
           100          105          110
Arg Gly Glu Leu Ala Cys Lys Tyr Gly Val Arg Ile Lys Ile Ile Gly
           115          120          125
Asp Leu Ser Leu Leu Asp Lys Ser Leu Leu Glu Asp Val Arg Val Ala
           130          135          140
Val Glu Thr Thr Lys Asn Asn Lys Arg Ala Thr Leu Asn Ile Cys Phe
           145          150          155          160
Pro Tyr Thr Gly Arg Glu Glu Ile Leu His Ala Met Lys Glu Thr Ile
           165          170          175
Val Gln His Lys Lys Gly Ala Ala Ile Asp Glu Ser Thr Leu Glu Ser
           180          185          190
His Leu Tyr Thr Ala Gly Val Pro Pro Leu Asp Leu Leu Ile Arg Thr
           195          200          205
Ser Gly Val Ser Arg Leu Ser Asp Phe Leu Ile Trp Gln Ala Ser Ser
           210          215          220
Lys Gly Val Arg Ile Glu Leu Leu Asp Cys Leu Trp Pro Glu Phe Gly
           225          230          235          240
Pro Ile Arg Met Ala Trp Ile Leu Leu Lys Phe Ser Phe His Lys Ser
           245          250          255
Phe Leu Asn Lys Glu Tyr Arg Leu Glu Glu Gly Asp Tyr Asp Glu Glu
           260          265          270
Thr Asn Gly Asp Pro Ile Asp Leu Lys Glu Lys Lys Leu Asn
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<210> 27

<211> 1032

<212> DNA

<213> *Saccharomyces cerevisiae*

<300>

<308> AB013498

<400> 27

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ttaagggtag ggccagtgcc tgaacatgtc tcctttatca tggatggtaa ccggagatat 240
gccaaagtcaa gaaggctacc agtaaaaaaa ggccatgaag ctggtgggtt aacgttacta 300
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caagtacatg aaaatgccac cattgaattt agtgatacgt tgtggccaaa ttttagcttc 840
tttgctatgt acctgatgat tctcaaatgg tccttctttt ccaccattca aaaatataat 900
gagaagaatc actcattgtt tgaaaaaata catgaaagcg ttccttcaat atttaaaaaa 960
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ggagatgaat aa 1032

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<210> 28

<211> 343

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 28

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 20          25          30

Phe Gln Arg Val Phe Ala Trp Val Met Ser Leu Ser Leu Phe Ser Trp
 35          40          45

Phe Tyr Val Asn Leu Gln Asn Ile Leu Ile Lys Ala Leu Arg Val Gly
 50          55          60

Pro Val Pro Glu His Val Ser Phe Ile Met Asp Gly Asn Arg Arg Tyr
 65          70          75          80

Ala Lys Ser Arg Arg Leu Pro Val Lys Lys Gly His Glu Ala Gly Gly
 85          90          95

Leu Thr Leu Leu Thr Leu Leu Tyr Ile Cys Lys Arg Leu Gly Val Lys
100          105          110

Cys Val Ser Ala Tyr Ala Phe Ser Ile Glu Asn Phe Asn Arg Pro Lys
115          120          125

Glu Glu Val Asp Thr Leu Met Asn Leu Phe Thr Val Lys Leu Asp Glu
130          135          140

Phe Ala Lys Arg Ala Lys Asp Tyr Lys Asp Pro Leu Tyr Gly Ser Lys
145          150          155          160

Ile Arg Ile Val Gly Asp Gln Ser Leu Leu Ser Pro Glu Met Arg Lys
165          170          175

Lys Ile Lys Lys Val Glu Glu Ile Thr Gln Asp Gly Asp Asp Phe Thr
180          185          190

Leu Phe Ile Cys Phe Pro Tyr Thr Ser Arg Asn Asp Met Leu His Thr
195          200          205

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Ile Arg Asp Ser Val Glu Asp His Leu Glu Asn Lys Ser Pro Arg Ile
 210 215 220
 Asn Ile Arg Lys Phe Thr Asn Lys Met Tyr Met Gly Phe His Ser Asn
 225 230 235 240
 Lys Cys Glu Leu Leu Ile Arg Thr Ser Gly His Arg Arg Leu Ser Asp
 245 250 255
 Tyr Met Leu Trp Gln Val His Glu Asn Ala Thr Ile Glu Phe Ser Asp
 260 265 270
 Thr Leu Trp Pro Asn Phe Ser Phe Phe Ala Met Tyr Leu Met Ile Leu
 275 280 285
 Lys Trp Ser Phe Phe Ser Thr Ile Gln Lys Tyr Asn Glu Lys Asn His
 290 295 300
 Ser Leu Phe Glu Lys Ile His Glu Ser Val Pro Ser Ile Phe Lys Lys
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 325 330 335
 Val Ser Val Thr Gly Asp Glu
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<210> 29
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